Figure 1

```
2588 GA TCAATCGCAT TCATTTTAAG AAATTATACC TTTTTAGTAC TTGCTGAAGA
2641 ATGATTCAGG GTAAATCACA TACTTTGTTT AGAGAGGCGA GGGGTTTAAC CCGAGTCACC
2701 CAGCTGGTCT CATACATAGA CAGCACTTGT GAAGGATTGA ATGCAGGTTC CAGGTGGAGG
2761 GAAGACGTGG ACACCATCTC CACTGAGCCA TGCAGACATT TTTAAAAGCT ATACACAAAA
2821 TTGTGAGAAG ACATTGGCCA ACTCTTTCAA AGTCTTTCTT TTTCCACGTG CTTCTTATTT
2881 TAAGCGAAAT ATATTGTTTG TTTCTTCCTA AAAAAAAAAA 2890
```

Figure 2

```
   1 CAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATC  60
  61 TCTGTTCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC 120
 121 ATGCCCTCTGCAGGAACACTTCCTTGGGTTCAGGGGATTATCTGTAATGCCAACAACCCC 180
   1 M  P  S  A  G  T  L  P  W  V  Q  G  I  I  C  N  A  N  N  P   20
 181 TGTTTCCGTTACCCGACTCCTGGGGAGGCTCCCGGAGTTGTTGGAAACTTTAACAAATCC 240
  21 C  F  R  Y  P  T  P  G  E  A  P  G  V  V  G  N  F  N  K  S   40
 241 ATTGTGGCTCGCCTGTTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCAGAAAGACACC 300
  41 I  V  A  R  L  F  S  D  A  R  R  L  L  L  Y  S  Q  K  D  T   60
 301 AGCATGAAGGACATGCGCAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA 360
  61 S  M  K  D  M  R  K  V  L  R  T  L  Q  Q  I  K  K  S  S  S   80
 361 AACTTGAAGCTTCAAGATTTCCTGGTGGACAATGAAACCTTCTCTGGGTTCCTGTATCAC 420
  81 N  L  K  L  Q  D  F  L  V  D  N  E  T  F  S  G  F  L  Y  H  100
 421 AACCTCTCTCTCCCAAAGTCTACTGTGGACAAGATGCTGAGGGCTGATGTCATTCTCCAC 480
 101 N  L  S  L  P  K  S  T  V  D  K  M  L  R  A  D  V  I  L  H  120
 481 AAGGTATTTTTGCAAGGCTACCAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 540
 121 K  V  F  L  Q  G  Y  Q  L  H  L  T  S  L  C  N  G  S  K  S  140
 541 GAAGAGATGATTCAACTTGGTGACCAAGAAGTTTCTGAGCTTTGTGGCCTACCAAGGGAG 600
 141 E  E  M  I  Q  L  G  D  Q  E  V  S  E  L  C  G  L  P  R  E  160
 601 AAACTGGCTGCAGCAGAGCGAGTACTTCGTTCCAACATGGACATCCTGAAGCCAATCCTG 660
 161 K  L  A  A  A  E  R  V  L  R  S  N  M  D  I  L  K  P  I  L  180
 661 AGAACACTAAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCCGAAGCCACAAAAACA 720
 181 R  T  L  N  S  T  S  P  F  P  S  K  E  L  A  E  A  T  K  T  200
 721 TTGCTGCATAGTCTTGGGACTCTGGCCCAGGAGCTGTTCAGCATGAGAAGCTGGAGTGAC 780
 201 L  L  H  S  L  G  T  L  A  Q  E  L  F  S  M  R  S  W  S  D  220
 781 ATGCGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC 840
 221 M  R  Q  E  V  M  F  L  T  N  V  N  S  S  S  S  S  T  Q  I  240
 841 TACCAGGCTGTGTCTCGTATTGTCTGCGGGCATCCCGAGGGAGGGGGGCTGAAGATCAAG 900
 241 Y  Q  A  V  S  R  I  V  C  G  H  P  E  G  G  G  L  K  I  K  260
 901 TCTCTCAACTGGTATGAGGACAACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 960
 261 S  L  N  W  Y  E  D  N  N  Y  K  A  L  F  G  G  N  G  T  E  280
```

961 GAAGATGCTGAAACCTTCTATGACAACTCTACAACTCCTTACTGCAATGATTTGATGAAG 1020
281 E D A E T F Y D N S T T P Y C N D L M K 300
1021 AATTTGGAGTCTAGTCCTCTTTCCCGCATTATCTGGAAAGCTCTGAAGCCGCTGCTCGTT 1080
301 N L E S S P L S R I I W K A L K P L L V 320
1081 GGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGGCAGGTCATGGCTGAGGTGAAC 1140
321 G K I L Y T P D T P A T R Q V M A E V N 340
1141 AAGACCTTCCAGGAACTGGCTGTGTTCCATGATCTGGAAGGCATGTGGGAGGAACTCAGC 1200
341 K T F Q E L A V F H D L E G M W E E L S 360
1201 CCCAAGATCTGGACCTTCATGGAGAACAGCCAAGAAATGGACCTTGTCCGGATGCTGTTG 1260
361 P K I W T F M E N S Q E M D L V R M L L 380
1261 GACAGCAGGGACAATGACCACTTTTGGGAACAGCAGTTGGATGGCTTAGATTGGACAGCC 1320
381 D S R D N D H F W E Q Q L D G L D W T A 400
1321 CAAGACATCGTGGCGTTTTTGGCCAAGCACCCAGAGGATGTCCAGTCCAGTAATGGTTCT 1380
401 Q D I V A F L A K H P E D V Q S S N G S 420
1381 GTGTACACCTGGAGAGAAGCTTTCAACGAGACTAACCAGGCAATCCGGACCATATCTCGC 1440
421 V Y T W R E A F N E T N Q A I R T I S R 440
1441 TTCATGGAGTGTGTCAACCTGAACAAGCTAGAACCCATAGCAACAGAAGTCTGGCTCATC 1500
441 F M E C V N L N K L E P I A T E V W L I 460
1501 AACAAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTATTGTGTTCACTGGA 1560
461 N K S M E L L D E R K F W A G I V F T G 480
1561 ATTACTCCAGGCAGCATTGAGCTGCCCCATCATGTCAAGTACAAGATCCGAATGGACATT 1620
481 I T P G S I E L P H H V K Y K I R M D I 500
1621 GACAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACCCTGGTCCTCGAGCT 1680
501 D N V E R T N K I K D G Y W D P G P R A 520
1681 GACCCCTTTGAGGACATGCGGTACGTCTGGGGGGGCTTCGCCTACTTGCAGGATGTGGTG 1740
521 D P F E D M R Y V W G G F A Y L Q D V V 540
1741 GAGCAGGCAATCATCAGGGTGCTGACGGGCACCGAGAAGAAAACTGGTGTCTATATGCAA 1800
541 E Q A I I R V L T G T E K K T G V Y M Q 560
1801 CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGCGGGTGATGAGCCGGTCAATG 1860
561 Q M P Y P C Y V D D I F L R V M S R S M 580
1861 CCCCTCTTCATGACGCTGGCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG 1920
581 P L F M T L A W I Y S V A V I I K G I V 600
1921 TATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACAGCATC 1980
601 Y E K E A R L K E T M R I M G L D N S I 620
1981 CTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTCTTGTGAGCGCTGGCCTGCTA 2040
621 L W F S W F I S S L I P L L V S A G L L 640
2041 GTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTTTGTC 2100
641 V V I L K L G N L L P Y S D P S V V F V 660

2101 TTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACACTCTTC 2160

SUBSTITUTE SHEET (RULE 26)

```
 661 F  L  S  V  F  A  V  V  T  I  L  Q  C  F  L  I  S  T  L  F  680
2161 TCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCC 2220
 681 S  R  A  N  L  A  A  A  C  G  G  I  I  Y  F  T  L  Y  L  P  700
2221 TACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC 2280
 701 Y  V  L  C  V  A  W  Q  D  Y  V  G  F  T  L  K  I  F  A  S  720
2281 CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTTGAGGAGCAG 2340
 721 L  L  S  P  V  A  F  G  F  G  C  E  Y  F  A  L  F  E  E  Q  740
2341 GGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCTGTGGAGGAAGATGGCTTCAAT 2400
 741 G  I  G  V  Q  W  D  N  L  F  E  S  P  V  E  E  D  G  F  N  760
2401 CTCACCACTTCGGTCTCCATGATGCTGTTTGACACCTTCCTCTATGGGGTGATGACCTGG 2460
 761 L  T  T  S  V  S  M  M  L  F  D  T  F  L  Y  G  V  M  T  W  780
2461 TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATTCCCAGGCCCTGGTATTTTCCTTGC 2520
 781 Y  I  E  A  V  F  P  G  Q  Y  G  I  P  R  P  W  Y  F  P  C  800
2521 ACCAAGTCCTACTGGTTTGGCGAGGAAAGTGATGAGAAGAGCCACCCTGGTTCCAACCAG 2580
 801 T  K  S  Y  W  F  G  E  E  S  D  E  K  S  H  P  G  S  N  Q  820
2581 AAGAGAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGAAGCTGGGCGTGTCC 2640
 821 K  R  I  S  E  I  C  M  E  E  E  P  T  H  L  K  L  G  V  S  840
2641 ATTCAGAACCTGGTAAAAGTCTACCGAGATGGGATGAAGGTGGCTGTCGATGGCCTGGCA 2700
 841 I  Q  N  L  V  K  V  Y  R  D  G  M  K  V  A  V  D  G  L  A  860
2701 CTGAATTTTTATGAGGGCCAGATCACCTCCTTCCTGGGCCACAATGGAGCGGGGAAGACG 2760
 861 L  N  F  Y  E  G  Q  I  T  S  F  L  G  H  N  G  A  G  K  T  880
2761 ACCACCATGTCAATCCTGACCGGGTTGTTCCCCCCGACCTCGGGCACCGCCTACATCCTG 2820
 881 T  T  M  S  I  L  T  G  L  F  P  P  T  S  G  T  A  Y  I  L  900
2821 GGAAAAGACATTCGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGGTCTGTCCCCAG 2880
 901 G  K  D  I  R  S  E  M  S  T  I  R  Q  N  L  G  V  C  P  Q  920
2881 CATAACGTGCTGTTTGACATGCTGACTGTCGAAGAACACATCTGGTTCTATGCCCGCTTG 2940
 921 H  N  V  L  F  D  M  L  T  V  E  E  H  I  W  F  Y  A  R  L  940
2941 AAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3000
 941 K  G  L  S  E  K  H  V  K  A  E  M  E  Q  M  A  L  D  V  G  960
3001 TTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTCAGGTGGAATGCAGAGAAAG 3060
 961 L  P  S  S  K  L  K  S  K  T  S  Q  L  S  G  G  M  Q  R  K  980
3061 CTATCTGTGGCCTTGGCCTTTGTCGGGGGATCTAAGGTTGTCATTCTGGATGAACCCACA 3120
 981 L  S  V  A  L  A  F  V  G  G  S  K  V  V  I  L  D  E  P  T  1000
3121 GCTGGTGTGGACCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA 3180
1001 A  G  V  D  P  Y  S  R  R  G  I  W  E  L  L  L  K  Y  R  Q  1020
3181 GGCCGCACCATTATTCTCTCTACACACCACATGGATGAAGCGGACGTCCTGGGGGACAGG 3240
1021 G  R  T  I  I  L  S  T  H  H  M  D  E  A  D  V  L  G  D  R  1040
3241 ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCCTGTTTCTGAAGAAC 3300
1041 I  A  I  I  S  H  G  K  L  C  C  V  G  S  S  L  F  L  K  N  1060
3301 CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT 3360
```

SUBSTITUTE SHEET (RULE 26)

```
1061 Q  L  G  T  G  Y  Y  L  T  L  V  K  K  D  V  E  S  S  L  S  1080
3361 TCCTGCAGAAACAGTAGTAGCACTGTGTCATACCTGAAAAAGGAGGACAGTGTTTCTCAG 3420
1081 S  C  R  N  S  S  S  T  V  S  Y  L  K  K  E  D  S  V  S  Q  1100
3421 AGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAGAGTGACACGCTGACCATCGATGTC 3480
1101 S  S  S  D  A  G  L  G  S  D  H  E  S  D  T  L  T  I  D  V  1120
3481 TCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCGGCTGGTGGAAGACATA 3540
1121 S  A  I  S  N  L  I  R  K  H  V  S  E  A  R  L  V  E  D  I  1140
3541 GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGGAGCCTTTGTGGAA 3600
1141 G  H  E  L  T  Y  V  L  P  Y  E  A  A  K  E  G  A  F  V  E  1160
3601 CTCTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 3660
1161 L  F  H  E  I  D  D  R  L  S  D  L  G  I  S  S  Y  G  I  S  1180
3661 GAGACGACCCTGGAAGAAATATTCCTCAAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAG 3720
1181 E  T  T  L  E  E  I  F  L  K  V  A  E  E  S  G  V  D  A  E  1200
3721 ACCTCAGATGGTACCTTGCCAGCAAGACGAAACAGGCGGGCCTTCGGGGACAAGCAGAGC 3780
1201 T  S  D  G  T  L  P  A  R  R  N  R  R  A  F  G  D  K  Q  S  1220
3781 TGTCTTCGCCCGTTCACTGAAGATGATGCTGCTGATCCAAATGATTCTGACATAGACCCA 3840
1221 C  L  R  P  F  T  E  D  D  A  A  D  P  N  D  S  D  I  D  P  1240
3841 GAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGGTCCTACCAGGTGAAA 3900
1241 E  S  R  E  T  D  L  L  S  G  M  D  G  K  G  S  Y  Q  V  K  1260
3901 GGCTGGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAATTGCC 3960
1261 G  W  K  L  T  Q  Q  Q  F  V  A  L  L  W  K  R  L  L  I  A  1280
3961 AGACGGAGTCGGAAAGGATTTTTTGCTCAGATTGTCTTGCCAGCTGTGTTTGTCTGCATT 4020
1281 R  R  S  R  K  G  F  F  A  Q  I  V  L  P  A  V  F  V  C  I  1300
4021 GCCCTTGTGTTCAGCCTGATCGTGCCACCCTTTGGCAAGTACCCCAGCCTGGAACTTCAG 4080
1301 A  L  V  F  S  L  I  V  P  P  F  G  K  Y  P  S  L  E  L  Q  1320
4081 CCCTGGATGTACAACGAACAGTACACATTTGTCAGCAATGATGCTCCTGAGGACACGGGA 4140
1321 P  W  M  Y  N  E  Q  Y  T  F  V  S  N  D  A  P  E  D  T  G  1340
4141 ACCCTGGAACTCTTAAACGCCCTCACCAAAGACCCTGGCTTCGGGACCCGCTGTATGGAA 4200
1341 T  L  E  L  L  N  A  L  T  K  D  P  G  F  G  T  R  C  M  E  1360
4201 GGAAACCCAATCCCAGACACGCCCTGCCAGGCAGGGGAGGAAGAGTGGACCACTGCCCCA 4260
1361 G  N  P  I  P  D  T  P  C  Q  A  G  E  E  E  W  T  T  A  P  1380
4261 GTTCCCCAGACCATCATGGACCTCTTCCAGAATGGGAACTGGACAATGCAGAACCCTTCA 4320
1381 V  P  Q  T  I  M  D  L  F  Q  N  G  N  W  T  M  Q  N  P  S  1400
4321 CCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTGTGTGTCCCCCAGGG 4380
1401 P  A  C  Q  C  S  S  D  K  I  K  K  M  L  P  V  C  P  P  G  1420
4381 GCAGGGGGGCTGCCTCCTCCACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTG 4440
1421 A  G  G  L  P  P  P  Q  R  K  Q  N  T  A  D  I  L  Q  D  L  1440
4441 ACAGGAAGAAACATTTCGGATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGC 4500
1441 T  G  R  N  I  S  D  Y  L  V  K  T  Y  V  Q  I  I  A  K  S  1460
4501 TTAAAGAACAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGT 4560
```

09736805.060200

1461 L K N K I W V N E F R Y G G F S L G V S 1480
4561 AATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAA 4620
1481 N T Q A L P P S Q E V N D A T K Q M K K 1500
4621 CACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTT 4680
1501 H L K L A K D S S A D R F L N S L G R F 1520
4681 ATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCAT 4770
1521 M T G L D T R N N V K V W F N N K G W H 1540
4741 GCAATCAGCTCTTTCCTGAATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAG 4800
1541 A I S S F L N V I N N A I L R A N L Q K 1560
4801 GGAGAGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAG 4860
1561 G E N P S H Y G I T A F N H P L N L T K 1580
4861 CAGCAGCTCTCAGAGGTGGCTCCGATGACCACATCAGTGGATGTCCTTGTGTCCATCTGT 4920
1581 Q Q L S E V A P M T T S V D V L V S I C 1600
4921 GTCATCTTTGCAATGTCCTTCGTCCCAGCCAGCTTTGTCGTATTCCTGATCCAGGAGCGG 4980
1601 V I F A M S F V P A S F V V F L I Q E R 1620
4981 GTCAGCAAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTGTCATCTACTGGCTC 5040
1621 V S K A K H L Q F I S G V K P V I Y W L 1640
5041 TCTAATTTTGTCTGGGATATGTGCAATTACGTTGTCCCTGCCACACTGGTCATTATCATC 5100
1641 S N F V W D M C N Y V V P A T L V I I I 1660
5101 TTCATCTGCTTCCAGCAGAAGTCCTATGTGTCCTCCACCAATCTGCCTGTGCTAGCCCTT 5160
1661 F I C F Q Q K S Y V S S T N L P V L A L 1680
5161 CTACTTTTGCTGTATGGGTGGTCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGTTC 5220
1681 L L L L Y G W S I T P L M Y P A S F V F 1700
5221 AAGATCCCCAGCACAGCCTATGTGGTGCTCACCAGCGTGAACCTCTTCATTGGCATTAAT 5280
1701 K I P S T A Y V V L T S V N L F I G I N 1720
5281 GGCAGCGTGGCCACCTTTGTGCTGGAGCTGTTCACCGACAATAAGCTGAATAATATCAAT 5340
1721 G S V A T F V L E L F T D N K L N N I N 1740
5341 GATATCCTGAAGTCCGTGTTCTTGATCTTCCCACATTTTTGCCTGGGACGAGGGCTCATC 5400
1741 D I L K S V F L I F P H F C L G R G L I 1760
5401 GACATGGTGAAAAACCAGGCAATGGCTGATGCCCTGGAAAGGTTTGGGGAGAATCGCTTT 5460
1761 D M V K N Q A M A D A L E R F G E N R F 1780
5461 GTGTCACCATTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGG 5520
1781 V S P L S W D L V G R N L F A M A V E G 1800
5521 GTGGTGTTCTTCCTCATTACTGTTCTGATCCAGTACAGATTCTTCATCAGGCCCAGACCT 5580
1801 V V F F L I T V L I Q Y R F F I R P R P 1820
5581 GTAAATGCAAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGAGGCGGGAAAGACAG 5640
1821 V N A K L S P L N D E D E D V R R E R Q 1840
5641 AGAATTCTTGATGGTGGAGGCCAGAATGACATCTTAGAAATCAAGGAGTTGACGAAGATA 5700
1841 R I L D G G G Q N D I L E I K E L T K I 1860
5701 TATAGAAGGAAGCGGAAGCCTGCTGTTGACAGGATTTGCGTGGGCATTCCTCCTGGTGAG 5760

```
1861 Y  R  R  K  R  K  P  A  V  D  R  I  C  V  G  I  P  P  G  E  1880
5761 TGCTTTGGGCTCCTGGGAGTTAATGGGGCTGGAAAATCATCAACTTTCAAGATGTTAACA 5820
1881 C  F  G  L  L  G  V  N  G  A  G  K  S  S  T  F  K  M  L  T  1900
5821 GGAGATACCACTGTTACCAGAGGAGATGCTTTCCTTAACAGAAATAGTATCTTATCAAAC 5880
1901 G  D  T  T  V  T  R  G  D  A  F  L  N  R  N  S  I  L  S  N  1920
5881 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTG 5940
1921 I  H  E  V  H  Q  N  M  G  Y  C  P  Q  F  D  A  I  T  E  L  1940
5941 TTGACTGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAGAA 6000
1941 L  T  G  R  E  H  V  E  F  F  A  L  L  R  G  V  P  E  K  E  1960
6001 GTTGGCAAGGTTGGTGAGTGGGCGATTCGGAAACTGGGCCTCGTGAAGTATGGAGAAAAA 6060
1961 V  G  K  V  G  E  W  A  I  R  K  L  G  L  V  K  Y  G  E  K  1980
6061 TATGCTGGTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6120
1981 Y  A  G  N  Y  S  G  G  N  K  R  K  L  S  T  A  M  A  L  I  2000
6121 GGCGGGCCTCCTGTGGTGTTTCTGGATGAACCCACCACAGGCATGGATCCCAAAGCCCGG 6180
2001 G  G  P  P  V  V  F  L  D  E  P  T  T  G  M  D  P  K  A  R  2020
6181 CGGTTCTTGTGGAATTGTGCCCTAAGTGTTGTCAAGGAGGGGAGATCAGTAGTGCTTACA 6240
2021 R  F  L  W  N  C  A  L  S  V  V  K  E  G  R  S  V  V  L  T  2040
6241 TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGA 6300
2041 S  H  S  M  E  E  C  E  A  L  C  T  R  M  A  I  M  V  N  G  2060
6301 AGGTTCAGGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGGAGATGGTTATACA 6360
2061 R  F  R  C  L  G  S  V  Q  H  L  K  N  R  F  G  D  G  Y  T  2080
6361 ATAGTTGTACGAATAGCAGGGTCCAACCCGGACCTGAAGCCTGTCCAGGATTTCTTTGGA 6420
2081 I  V  V  R  I  A  G  S  N  P  D  L  K  P  V  Q  D  F  F  G  2100
6421 CTTGCATTTCCTGGAAGTGTTCCAAAAGAGAAACACCGGAACATGCTACAATACCAGCTT 6480
2101 L  A  F  P  G  S  V  P  K  E  K  H  R  N  M  L  Q  Y  Q  L  2120
6481 CCATCTTCATTATCTTCTCTGGCCAGGATATTCAGCATCCTCTCCCAGAGCAAAAAGCGA 6540
2121 P  S  S  L  S  S  L  A  R  I  F  S  I  L  S  Q  S  K  K  R  2140
6541 CTCCACATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAGTATTTGTGAACTTT 6600
2141 L  H  I  E  D  Y  S  V  S  Q  T  T  L  D  Q  V  F  V  N  F  2160
6601 GCCAAGGACCAAAGTGATGATGACCACTTAAAAGACCTCTCATTACACAAAAACCAGACA 6660
2161 A  K  D  Q  S  D  D  D  H  L  K  D  L  S  L  H  K  N  Q  T  2180
6661 GTAGTGGACGTTGCAGTTCTCACATCTTTTCTACAGGATGAGAAAGTGAAAGAAAGCTAT 6720
2181 V  V  D  V  A  V  L  T  S  F  L  Q  D  E  K  V  K  E  S  Y  2200
6721 GTATGAAGAATCCTGTTCATACGGGGTGGCTGAAAGTAAAGAGGGACTAGACTTTCCTTT 6780
2201 V  *
6781 GCACCATGTGAAGTGTTGTGGAGAAAAGAGCCAGAAGTTGATGTGGGAAGAAGTAAACTG 6840
6841 GATACTGTACTGATACTATTCAATGCAATGCAATTCAATG                       6880
```

Figure 3

5' 1 GTACCCCCCT TGCCTGGTTG ATCCTCAGGG TTCTACTTAG AATGCCTCGA

```
  51  AAAGTCTTGG CTGGACACCC ATGCCCAGTC TTTCTGCAGG GTCCCATTGG
 101  GGTTAACCTT CTCATTTCAT CCCATGTGAA CCAGGCCAGG CCCATCAGGG
 151  TTTGGCAACC CCCTGATGCA GTGGTTGCTG CCAGGTGACA GGAGCAAGCC
 201  TGCAGCTGCT GGGGGGCCAT GCAGAGACAG CCTGCCAGAG GGGAGACCAC
 251  CTGGGGAGGC CAGAGCCGTG GAGACAGCAA GAGACCAGGG GCTGAGGACA
 301  GAGTAGTACA GGTCTTTGGT CCCAGTAGTC CTGAAACCAC TGCACTCCGA
 351  ACCTTTCTGT ACTTAGCTTA AGCCAGTTGG AGTTTCTGTC CTTTACAACC
 401  AAGAGCCTTG ATAGGAATGG GGTCCTGTGC TACGCTACTG TTGGCTTCTT
 451  TCCCGATCGG GCGCTGGAGG GGAACACAGC AGTGACTACA GTGGGATGCT
 501  TACTCGGTGC TGGGCATGCT AGAAAGTGCT TGCCATGCCT TATTTCCCAC
 551  GTGGTGGGGA TTTTGACCCC ACCTGTACAG ACAGATAAGT GAGGACCCTT
 601  TTCACCTTAT CCTGCAACAG AAAATCCAGC AGCCAAAGCC AACAAGGGCC
 651  CAGCATAGCA TCTTCCCTCT CTGACTTCAT CCTCACGCTC CACACACCAT
 701  CCCCCTGGCC ATTCCCAGCA GCCCAGTAAG CACTGCCTCA CACTTCCAGT
 751  TCCGGACCAG CCAGGATGGC CAGGCTGGAT GGGGGCCATC CACCGGCTGA
 801  AGCCAATTGC CTATTCTCGA GCTGAAGGTG AATCAATCCC GCATAAATCT
 851  TCGGGCAGAG AACTNGGGTG GGGGGTAGAA GAGGGGGAAT GTCTAGAAGG
 901  AAATTCTGGG GCACATTCCT GGAAGTGAGG AGGATGGATA TTGGACAGAA
 951  ATTATGTCAT TGCAGGCACC CTCACTTGCC CTGGCCACAT GGACAGTTCC
1001  TCCCCGGCTG TGTTCCGNGC CTCCTCTCGT GCTCCAGGGC CTGTCTGTTC
1051  CTGGAGCGAG ATGGGTCCCA GGGCTGGGCA CCAGTCCCCA TCTCCAGCCA
1101  TCAGGCACTT TCCTCTCTGT GTTTTGGCGT AAACACNTCC CTAGGTTTGT
1151  GGATCTGAAT CCTCTTCCCA ACACACTCAA GCTTTGCTGG GCCTCCCTGC
1201  AGTGTATGTT TAAGGCACCA CACAGCCTCC AAGGCCTGGC ACCCGGGCAG
1251  TGGCCACCTG GTAAACACAG CAGTCAGATT TCCTCATTTC AGCCAAGTGT
1301  AAAATCAAGG TAATGGATCT ACNCTTTTTT TTTTNTNTTT TTTCCAGGGG
1351  GNTNNTTTTT TTTTGAGACG GAGTCTCACT CTGTCANCCC CGGTCTGGAG
1401  TGCAGTGGCT CAATCTCGGC TCANCTGGCA AGCTCCGCCT CCCAGGTTCA
1451  TGCCATTCTC CTGCCTCAGC CTACATAGTA GCTGGGACTA CAGGTGCCCG
1501  CCACCACACC TAGCTAATTT TTTGTATTTT TAGTAGAGAC GGGGTTTCAT
1551  CATGTTAGCC AGGATGGTCT CGATCTCCTG ACCTCCCAAA GTGGTGGGAG
1601  TTACAGGTGT GAGCCACTGC GCNCCGGCTG GATGACTCTT GAGACAACAC
1651  CATTCAGACA AAGGCAAGGC CTCCCACTTA AACTCATAAC CGTGTCTCCT
1701  TTCTCTCCTT CGATTTGAGC GGCTGAATTT GGTTACAGTC ATCTGACCTG
1751  TGGGTGTGAA NGTCCACCTG CCTGGCATAA AAAGCTGTGC CTCCTTTCTA
1801  GGTGAGGAGA AAGAGAGAGA CCTGGCTCAT CTGAGGTGTG GTTGGGAGGG
1851  GGGACCCAGG TGTGCTGGAA ATGAAAAGAA ATGCATTCCT GTTTTTTCGT
1901  CCCAACATGC AAACAACTGA ACAAAAGCAT TAGGGCCTGA GACTGGGAGT
1951  AAAGAATTCC TTGTCACCAT GGATACCAGG AAATGGCCCC ACTTATATAT
2001  AATAAGGGCT TTAGAGATGC TGGACCATCT GATATTCCAG CCTGGGGCCA
2051  CATGGGAGTG TGCCCTGGTG TTATTCCTTA TACAGTTCCA TGAACATGGC
2101  TCTGGAAACA CCTCTGTCTG CAGAAAATGA GGCTTTTCTT TTTTTGTTCG
```

SUBSTITUTE SHEET (RULE 26)

```
2151  GGGGTGAACA GAGGGCAGAG GCCTGGGCAT CTTCACTCAG CACCCCTTTG
2201  TAACCCAGCA CTTAGCACCA TGGCTGGCGC ACAGCAATGT CACATGTGTG
2251  AGTGCACACG ATGCCTCACT GCCAGGGGTC ACCCCACACC GGTGCTGTTG
2301  GGGGCGTTGG AGTGGTTATC TCTTCTTTAG TCCTCAAGCT CCTACCTGGC
2351  AGAGAGCTGC CCAACACCGT CGGGGTGGGG TGGGCGGGAA GGGAAGAAGC
2401  AGCAGCAAGA AAGAAGCCCC CTGGCCCTCA CTCTCCCTCC CTGGACGCCC
2451  CCTCTTCGAC CCCATCACAC AGCCGCTTGA GCCTTGGAGN CAGTGGATTT
2501  CCGAGCCTGG GAACCCCCGG CGTCTGTCCC GGTGTCCCCC GCAGCCTCAC
2551  CCNCGTGCTG GCCCAGCCCC CGCGAGTTCG GGACCCGGGG TTTCCGGGGT
2601  GGCAGGGGGT TCCCATGCCG CCTGCGAGGC CTCGGCTCGG GCCGCTCCCG
2651  GAACCTGCAC TTCAGGGGTC CTGGTCCGCC GCCCCCAGCA GGAGCAAAAC
2701  AAGAGCACGC GCACCTGCCG GCCCGCCCGC CCCCTTGGTG CCGGCCAATC
2751  GCGCGCTCGG GGCGGGGTCG GGCGCGCTGG AACCAGAGCC GGAGCCGGAT
2801  CCCAGCCGGA GCCCAAGCGC AGCCCGCACC CCGCGCAGCG GCTGAGCCGG
2851  GAGCCAGCGC AGCCTCGGCC CCGCAGCTCA AGCCTCGTCC CCGCCGCCNG
2901  CCGCCGCACG CCGCCGCCGC CGCCCCCGGG GCATGGCTGT CTGATGGCCG

                        EXON1/INTRON 1
2951  CTTTCTCGGT CGGCACCGCC ATGGTGAGTG AGCGCATCCT TCGTCCGCCG
3001  GGAACGGTTT TATTTTCAAG GAGAGCAGGA AACACACAAA GACTCGCAAG
3051  CTCGACCTGA CACCCCTCCC AGGAGCGCGT CCTCTGGGGC GCTGACCCAG
3101  GGGCACCCTA GAGTGGCGCC CGGCTCCGAT CGCTGCCCCT NNCCCCTCCG
3151  CCAGGGCCAC CTGGGAGCCT CGGGGATGCC CCTTGCACCG GCAGAGNGCA
3201  CGGACTAGGT GGAGGGGNCC GGGATTGGGG CGGGGGGCAG NCAGTTGCCC
3251  TACAAGTTGG ACCGATGGCC TTGACCTGAT GGCTTCTGGG CGGGGGGCGT
3301  GGGGAGCTGG GGACCCGGAG CGCACTGGGG ACTGGGGAGG GGCCGCAGCT
3351  TGGGCCGGAG GGAAGAGGGG ACTTGAAGAA GGGGAGCCCC GCGCGCGCGG
3401  CTGTGGGCTT GGGGACCGGG GACTTCTCGC GCCATCCCCA GGAACGCCAG
3451  GCAAGGTCTG GGGAACAAAA GAGGAAGCTG CCCCCAGAGA GCCGGAGCTC
3501  GACTGNACTC CC 3'
```

Figure 4

```
5'
   1  CTTGGTGCCG CATGCATCGT GGTGCTCATC TTTCTGGCCT TCCAGCAGAG
  51  GGCATATGTG GCCCCTGCCA ACCTGCCTGC TCTCCTGCTG TTGCTACTAC
 101  TGTATGGCTG GTCGATCACA CCGCTCATGT ACCCAGCCTC CTTCTTCTTC
 151  TCCGTGCCCA GCACAGCCTA TGTGGTGCTC ACCTGCATAA ACCTCTTTAT
 201  TGGCATCAAT GGAAGCATGG CCACCTTTGT GCTTGAGCTC TTCTCTGATC
 251  AGAAGCTGCA GGAGGTGAGC CGGATCTTGA AACAGGTCTT CCTTATCTTC
 301  CCCACTTCTG CTTGGGCCGG GGGCTTATTG ACATGGTGCG GNAACCAGGC
 351  CATGGCTGAT GCCTTTGANC CCTTGGGAAA AAGGCAGTTC AAGTACCCTG
```

```
 401  NCTTGGAAGG TGGCGGAAGA ACCTTTTGGC ATGGGAACAG GGCCCCTTTT
 451  CCTTCTCTTC ACACTANTGT TCAAGCACCG AAGCCAACTC NTGCCACAAG
 501  CCCAGGTAAG GTCTCTGCCA CTCCTGGAGA GAGACGAGGA TGTAGCCCGT
 551  GAACGGGAGC GGGTGGTCCA AGGAGCCACC CAGGGGGATG TGTTGGTGCT
 601  GAGGAACTTG ACCAAGGTAT ACCGTGGGCA GAGGATGCCA GCTGTTGACC
 651  GCTTGTGCCT GGGGATTCCC CCTGGTGAGT GTTTTGGGCT GCTGGGTGTG
 701  AACGGAGCAG GGAAGACGTC CACGTTTCGC ATGGTGACGG GGGACACATT
 751  GGCCAGCAGG GGCGAGGCTG TGCTGGCAGG CCACAGCGGG CCCGGGAACC
 801  CAGTGTGCGC ACCTCNAGGG CAGGCNCAGC GTGGCCCGGG AACCCAGTGC
 851  TGCGCACCTA AGCATGGGAT ACTGCCCTNA ATCCGATGCC ATCTTTGAGC
 901  TGCTGACGGG CCGCGAGCAC CTGGAGCTGC TTGCGCGCCT GCGCGGTGTC
 951  CCGGAGGCCC AGGTTGCCCA NACCGNTGGC TCGGGCCTGG CGCGTCTGGG
1001  ACTCTCATGG TACGCAGACC GGCCTGCAGG CACCTACAGG AACCTGCCCG
1051  GGCGGCCGCT CGAGCCCNTA NNTGAAGTA  3'
```

Figure 4b

```
...CTCCTGCCAC AGTTAGTGAG GTCTATGGAG AGGGTGGCAG GGGCCAAGGA
      CCTACTTTAA GCCCACAGAT ATTCTGTCCC CAGGCCCAGG GTGAGGTCTC...
```

SUBSTITUTE SHEET (RULE 26)

Figure 5

CDNA-sequences of lipid sensitive Genes:

ABCB9, ABCA6, ABCC4, ABCA1, ABCD2, ABCB1, ABCB4, ABCC2, ABCD1, ABCC1, ABCB6, ABCB11, ABCG2, ABCC5, ABCA5, ABCG1, ABCA3

ABCB9 GENBANK:U66676

GCCAATGNCACGGTTTCATCATGGAACTCCAGGACGGCTACAGCACAGAGACAGGGGAGA
AGGGCGCCCAGCTGTCAGGTGGCCAGAAGCAGCGGGTGGCCATGGCCGNGGCTCTGGTGC
GGAACCCCCCAGTCCTCATCCTGGATGAAGCCACCAGCGCTTTGGATGCCGAGAGCGAGT
ATCTGATCCAGCAGGCCATCCATGGCAACCTGTCAGAAGCACACGGTACTCATCATCGCG
CACCGGCTGAGCACCGTGGAGCACGCGCACCTCATTGTGGTGCTGGACAAGGGCCGCGTA
GTGCAGCAGGGCACCCACCAGCAGCTTGCTTGCCCCAGGGCGGGCTTTTACGGCAAGCTN
GTTGCAGCGGCAGATGTGGGGTTTCAAGGCCGCAGACTTCACAGCTGGCCACAACGAGCC
TGTAGCCAACGGGTCACAAGGCCTGATGGGGGGCCCCTCCTTCGCCCGGTGGCAGAGGAC
CCGGTGCCTGCCTGGCAGATGTGCCCACGGAGGTTTCCAGCTGCCCTACCGAGCCCAGGC
CTGCAGCACTGAAAGACGACCTGCCATGTCCCATGATCACCGCTTNTGCAATCTTGCCCC
TGGTCCCTGCCCCATTCCCAGGGCACTCTTACCCCNNNCTGGGGGATGTCCAAGAGCATA
GTCCTCTCCCCATACCCCTCCAGAGAAGGGGCTTCCCTGTCCGGAGGGAGACACGGGGAA
CGGGATTTTCCGTCTCTCCCTCTTGCCAGCTCTGTGAGTCTGGCCAGGGCGGGTAGGGAG
CGTGGAGGGCATCTGTCTGCCAATTGCCCGCTGCCAATCTAAGCCAGTCTCACTGTGACC
ACACGAAACCTCAACTGGGGGAGTGAGGAGCTGGCCAGGTCTGGAGGGGCCTCAGGTGCC
CCCAGCCCGGCACCCAGCTTTCGCCCCTCGTCAATCAACCCCTGGCTGGCAGCCGCCCTC
CCCACACCCGCCCCTGTGCTCTGCTGTCTGGAGGCCACGTGGACCTTCATGAGATGCATT
CTCTTCTGTCTTTGGTGGANGGATGGTGCAAAGCCCAGGATCTGGCTTTGCCAGAGGTT
GCAACATGTTGAGAGAACCCGGTCAATAAAGTGTACTACCTCTTACCCCT

ABCA6 GENBANK:U66680

TCTTAGATGAGAAACCTGTTATAATTGCCAGCTGTCTACACAAAGAATATGCAGGCCAGA
AGAAAAGTTGCTTTTCAAAGAGGAAGAAGAAAATAGCAGCAAGAAATATCTCTTTCTGTG
TTCAAGAAGGTGAAATTTTGGGATTGCTAGGACCCAATGGTGCTGGAAAAAGTTCATCTA
TTAGAATGATATCTGGGATCACAAAGCCAACTGCTGGAGAGGTGGAACTGAAAGGCTGCA
GTTCAGTTTTGGGCCACCTGGGGTACTGCCCTCAAGAGAACGTGCTGTGGCCCATGCTGA
CGTTGAGGGAACACCTGGAGGTGTATGCTGCCGTCAAGGGGCTCAGGAAAGCGGACGCGA
GGCTCGCCATCGCAAGATTAGTGAGTGCTTTCAAACTGCATGAGCAGCTGAATGTTCCTG
TGCAGAAATTAACAGCAGGAATCACGAGAAAGTTGTGTTTTGTGCTGAGCCTCCTGGGAA
ACTCACCTGTCTTGCTCCTGGATGAACCATCTACGGGCATAACCCCACAGGGCAGCAGCA
AATGTTGGCAGGCAATCCAGGCAGTCGTTAAAAACACAGAGAGAGGTGTCCTCCTGACCA
CCCATAACCTGGCTGAGGCGGAAGCCTTGTGTGACCGTGTGGCCATCATGGTGTCTGGAA
GGCTTAGATGCATTGGCTCCATCCAACACCTGAAAAACAAACTTGGCAAGGATTACATTC
TAGAGCTAAAAGTGAAGGAAACGTCTCAAGTGACTTTGGTCCACACTGAGATTCTGAAGC

TTTTCCCACAGGCTGCAGGGCAGGAAAGGTATTCCTCTTTGTTAACCTATAAGCTGCCCC
GTGGCAGACGTTTACCCTCTATCACAGACCTTTCACAAATTAGAAGCAGTGAAAGCATAA
CTTTAACCTGGAAGAATACAGCCTTTCTCCAGTGCACACTGGANAAGGTNTCCTTANAAC
CTTCCTAAANAACAGGAAGTTAGGAAATTTTGAATGAAAANNNACCNCCCCCCCTCATTC
AGGTGGAACCTTAAAACCTCAAACCTAGTAATTTTTTGTTGATCTCCTATAAAACTTATG
TTTTATGTAATAATTAATAGTATGTTTAATTTTAAAGATCATTTAAAATTAACATCAGGT
ATATTTTGTAAATTTAGTTAACAAATACATAAATTTTAAAATTATTCTTCCTCTCAAACA
TAGGGGTGATAGCAAACCTGTGATAAAGGCAATACAAAATATTAGTAAAGTCACCCAAAG
AGTCAGGCACTGGGTATTGTGGAAATAAAACTATATAAACTTAA

ABCC4 GENBANK:U66682

ATGGATAAGTTTATACTAGTGTTGGCACATGGCGGCATGTATAGATATACTAGGAGGACC
TAGTTGTATTCCTTGTATGAAAAAGCGTCCCTGGTACTACAATAAGTCTTTCGTGAAAGG
AGTGTAATCCTAACAACAACTCAGGAAAGTATTTTGAAAAGAATACTGGATAAGGAAAAA
CCTGCAGCTACTCCTGCTATTTCAAGACATTGCCTACAAGTGGTTGGTGTGGTCTCTGTG
GCTGTGGCCGTGATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATT
TTTCTTCGGCGATATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAAGT
GAGTATGGAAACTCGGGTTGGTATAGACATGCTAGCTAGTTTCCATTTATGCCATAAATT
ACAGAGACCCCCTGAAATTCGGCAGACTCTGTCTTCCAGAATTTCTCTAACATTAGGTAA
TTGAACGTATTGGCCATTATGAATCATTGTGTCCCTTAGAGCATGTGGAATTGATAGCCT
GCAACGTGTAACTTTGCATTTGGAATAAGGAAGGAGTGAAGGCCATATGGGGAGTAATAT
TCTACAGGAATGTCAGCACTGTGAAGACAGGGACTC

ABCA1 Acc.Nr.: AJ012376 GENBANK:HSA012376

CAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATC
TCTGTTCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC
ATGCCCTCTGCAGGAACACTTCCTTGGGTTCAGGGGATTATCTGTAATGCCAACAACCCC
TGTTTCCGTTACCCGACTCCTGGGGAGGCTCCCGGAGTTGTTGGAAACTTTAACAAATCC
ATTGTGGCTCGCCTGTTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCAGAAAGACACC
AGCATGAAGGACATGCGCAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA
AACTTGAAGCTTCAAGATTTCCTGGTGGACAATGAAACCTTCTCTGGGTTCCTGTATCAC
AACCTCTCTCTCCCAAAGTCTACTGTGGACAAGATGCTGAGGGCTGATGTCATTCTCCAC
AAGGTATTTTTGCAAGGCTACCAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA
GAAGAGATGATTCAACTTGGTGACCAAGAAGTTTCTGAGCTTTGTGGCCTACCAAGGGAG
AAACTGGCTGCAGCAGAGCGAGTACTTCGTTCCAACATGGACATCCTGAAGCCAATCCTG
AGAACACTAAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCCGAAGCCACAAAAACA
TTGCTGCATAGTCTTGGGACTCTGGCCCAGGAGCTGTTCAGCATGAGAAGCTGGAGTGAC
ATGCGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC
TACCAGGCTGTGTCTCGTATTGTCTGCGGGCATCCCGAGGGAGGGGGGCTGAAGATCAAG
TCTCTCAACTGGTATGAGGACAACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG

AGAATTCTTGATGGTGGAGGCCAGAATGACATCTTAGAAATCAAGGAGTTGACGAAGATA
TATAGAAGGAAGCGGAAGCCTGCTGTTGACAGGATTTGCGTGGGCATTCCTCCTGGTGAG
TGCTTTGGGCTCCTGGGAGTTAATGGGGCTGGAAAATCATCAACTTTCAAGATGTTAACA
GGAGATACCACTGTTACCAGAGGAGATGCTTTCCTTAACAGAAATAGTATCTTATCAAAC
ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTG
TTGACTGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAGAA
GTTGGCAAGGTTGGTGAGTGGGCGATTCGGAAACTGGGCCTCGTGAAGTATGGAGAAAAA
TATGCTGGTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC
GGCGGGCCTCCTGTGGTGTTTCTGGATGAACCCACCACAGGCATGGATCCCAAAGCCCGG
CGGTTCTTGTGGAATTGTGCCCTAAGTGTTGTCAAGGAGGGGAGATCAGTAGTGCTTACA
TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGA
AGGTTCAGGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGGAGATGGTTATACA
ATAGTTGTACGAATAGCAGGGTCCAACCCGGACCTGAAGCCTGTCCAGGATTTCTTTGGA
CTTGCATTTCCTGGAAGTGTTCCAAAAGAGAAACACCGGAACATGCTACAATACCAGCTT
CCATCTTCATTATCTTCTCTGGCCAGGATATTCAGCATCCTCTCCCAGAGCAAAAAGCGA
CTCCACATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAGTATTTGTGAACTTT
GCCAAGGACCAAAGTGATGATGACCACTTAAAAGACCTCTCATTACACAAAAACCAGACA
GTAGTGGACGTTGCAGTTCTCACATCTTTTCTACAGGATGAGAAAGTGAAAGAAAGCTAT
GTATGAAGAATCCTGTTCATACGGGGTGGCTGAAAGTAAAGAGGGACTAGACTTTCCTTT
GCACCATGTGAAGTGTTGTGGAGAAAAGAGCCAGAAGTTGATGTGGGAAGAAGTAAACTG
GATACTGTACTGATACTATTCAATGCAATGCAATTCAATG
ABCD2 Acc.Nr.: AJ000327 GENBANK:HSALDR
AAAACACAACAGTGGAAGAGAAACGCTGCATACTATGGGACGCTGTAGGACTTTCTAAAA
CATTTGCTGGGGATTTCTGTGAAGCATGATCTTTTAAACGAATTCTTTTGGAAGCCGGTT
TGGGTAACTGGGAAAATGACACATATGCTAAATGCAGCAGCTGATCGAGTGAAATGGACC
AGATCGAGTGCTGCTAAGAGGGCTGCCTGCCTGGTGGCTGCGGCATATGCTCTGAAAACC
CTCTATCCCATCATTGGCAAGCGTTTAAAGCAATCTGGCCACGGGAAGAAAAAAGCAGCA
GCTTACCCTGCTGCAGAGAACACAGAAATACTGCATTGCACCGAGACCATTTGTGAAAAA
CCTTCGCCTGGAGTGAATGCAGATTTCTTCAAACAGCTACTAGAACTTCGGAAAATTTTG
TTTCCAAAACTTGTGACCACTGAAACAGGGTGGCTCTGCCTGCACTCAGTGGCTCTAATC
TCAAGAACCTTTCTTTCTATCTATGTGGCTGGTCTGGATGGAAAAATCGTGAAAAGCATT
GTGGAAAAGAAGCCTCGGACTTTCATCATCAAATTAATCAAGTGGCTTATGATTGCCATC
CCTGCTACCTTCGTCAACAGTGCAATAAGGTACCTGGAATGCAAATTGGCTTTGGCCTTC
AGAACTCGCCTAGTAGACCACGCCTATGAAACCTATTTTACAAATCAGACTTATTATAAA
GTGATCAATATGGATGGGAGGCTGGCAAACCCTGACCAATCTCTTACGGAGGATATTATG
ATGTTCTCCCAATCTGTGGCTCACTTGTATTCCAATCTGACCAAACCTATTTTAGATGTA
ATGCTGACCTCCTATACACTCATTCAAACTGCTACATCCAGAGGAGCAAGCCCAATTGGG
CCCACCCTACTAGCAGGACTTGTGGTGTATGCCACTGCTAAAGTGTTAAAAGCCTGTTCT
CCCAAATTTGGCAAACTGGTGGCAGAGGAAGCACATAGAAAAGGCTATTTGCGGTATGTG

CACTCGAGAATTATAGCCAATGTAGAAGAAATTGCCTTTTACAGAGGACATAAGGTAGAA
ATGAAACAACTTCAGAAAAGTTACAAAGCTTTAGCAGATCAGATGAACCTCATTTTATCC
AAACGTTTGTGGTACATCATGATAGAACAGTTCCTGATGAAGTATGTTTGGAGCAGCAGT
GGACTAATTATGGTGGCTATACCTATTATCACTGCAACTGGCTTTGCAGATGGTGAGGAT
GGCCAAAAGCAAGTTATGGTTAGTGAACGGACAGAAGCCTTTACCACTGCTCGAAATTTA
CTGGCCTCTGGAGCTGATGCTATTGAAAGGATTATGTCTTCATACAAAGAGGTCACTGAA
TTAGCAGGCTACACTGCTCGAGTGTACAATATGTTTTGGGTCTTTGATGAAGTAAAAAGA
GGCATTTATAAGAGAACTGCTGTCATTCAAGAATCTGAAAGCCATAGCAAGAATGGAGCT
AAGGTAGAATTACCTCTCAGTGACACATTGGCAATTAAAGGAAAAGTTATTGATGTGGAT
CACGGAATTATTTGTGAAAATGTTCCCATAATTACACCAGCAGGAGAAGTGGTGGCTTCC
AGGCTAAACTTCAAAGTAGAAGAAGGAATGCATCTTTTGATAACTGGTCCCAATGGTTGT
GGGAAAAGTTCTCTCTTCAGAATTCTAAGTGGGCTCTGGCCTGTGTATGAAGGAGTCCTC
TATAAACCACCTCCTCAACATATGTTTTATATTCCACAAAGGCCATATATGTCTCTTGGA
AGTCTTCGGGATCAAGTCATTTACCCTGATTCAGTGGATGATATGCATGATAAAGGTTAT
ACAGACCAAGATCTGGAACGTATCCTACACAATGTCCATCTCTATCACATAGTTCAAAGA
GAAGGAGGATGGGATGCTGTTATGGACTGGAAAGATGTCCTGTCAGGAGGGGAAAAGCAA
AGAATGGGCATGGCTCGTATGTTTTATCATAAACCAAAATATGCCTTGCTGGATGAATGT
ACCAGTGCTGTCAGCATTGATGTCGAAGGAAAGATATTTCAGGCTGCAAAAGGGGCTGGA
ATTTCCTTACTGTCTATAACACACAGACCTTCTCTTTGGAAATACCACACACATTTATTA
CAGTTTGATGGTGAAGGAGGTTGGCGCTTTGAACAATTGGATACTGCTATCCGTTTGACA
TTGAGTGAAGAAAAACAAAAGCTAGAATCTCAGCTAGCTGGAATTCCCAAAATGCAGCAG
AGACTCAATGAACTATGTAAAATTTTGGGAGAAGACTCAGTGCTGAAAACAATTAAAAAT
GAAGATGAGACATCTTAATTTGTTTTGACATATTTTAAAAAGTTAATTATTAGATAAAGG
CTCAAAGACATTCTGTTATACTGCATGAAGTATGTTAAGCTAAGCACAGAGAAAAAAAGG
CAGCAAGACATGTTTTATAAGATTTTAGCATTAAGGAAGTATATGATCTGACTTTTCAGA
AGAAAATAAACAAATGCATTATGTAAGGTCAGTCATTATGACTTATACTAATTCCTAGTG
AAGGCCTAATGCACTTGTAAAACAGGATTTTCTAGGTGAATTCCTGATGAATACCAGATT
TACTATGTATATGTGGTGTGTCTGAAGTTCTTAACAAACATGGGCAATATTCTGGAAATG
AAACAAGTTATAACTGAGCACCATTTGGGTTGATACCAAGTGCATAAGATTCAAACTTTG
AGTGACATTTAGTCCATTTATGGTTGATATTAGGTTTAATACCTAGAATTCAAATTGATT
ATTGCTAGTGGCCAACTAAACCTGTACAAAATAGCTGACAGTTTTATAACTAATTTCAAT
ATAAAAATTGTTTTAATGGCATTTGTTGAAAGAAAAAAGCATGGCTAAAATGTATCAAAT
GCCNTATTTTTAAATTTTGGACTTTAAGCATCTTAATGAGGGCATATAACAAATTAATTT
TAGTACAATCTTAAATATTTTTAATAAATCCTTTCATTTTAAAAAGAGAATTGCCAATAC
AGAAAAGGAGTATCCAAACAATGTCTCAACCTGATAATTTCCTTAGCAGAATTACCTATT
GCAACTTCTGTTCAGAAATACACAGCTTGTTTTTTTGCCCAAGGATGAGTCTACATTTTA
AGAACTGCAATGGTATAAAGGAACTTAAGGATTCTGAGAATCATAGTAATAACATACATT
GGAATAGTACTTTATAATTTACAATCCCCATTTACATCATTTCACCTTAATGTTGAGGAC
AATGTTTTGAAACAAATACTATTTTTCCTACTTTGCTTTTGAGAAAATTGACACTCAGAC

SUBSTITUTE SHEET (RULE 26)

TTGCCCTAATCATGCACTTTACTTAAGGAAAGATCGAGAAATCAAATGAAGTTCTCCTGA
CTCTCTGGTTTAGTGCTCTTTTGTTATTATCCTTTAAATCAAACTGGGCTATAATAGCAA
TAAAAGTTAGACGAAGTGTAGAAAATAAAATAAATTTCATAATGTTAAAAAAAAAAAAAA
AAAAAAA

ABCB1 Acc.Nr. M14758 GENBANK:HUMMDR1

CCTACTCTATTCAGATATTCTCCAGATTCCTAAAGATTAGAGATCATTTCTCATTCTCCT
AGGAGTACTCACTTCAGGAAGCAACCAGATAAAAGAGAGGTGCAACGGAAGCCAGAACAT
TCCTCCTGGAAATTCAACCTGTTTCGCAGTTTCTCGAGGAATCAGCATTCAGTCAATCCG
GGCCGGGAGCAGTCATCTGTGGTGAGGCTGATTGGCTGGGCAGGAACAGCGCCGGGGCGT
GGGCTGAGCACAGCGCTTCGCTCTCTTTGCCACAGGAAGCCTGAGCTCATTCGAGTAGCG
GCTCTTCCAAGCTCAAAGAAGCAGAGGCCGCTGTTCGTTTCCTTTAGGTCTTTCCACTAA
AGTCGGAGTATCTTCTTCCAAGATTTCACGTCTTGGTGGCCGTTCCAAGGAGCGCGAGGT
CGGGATGGATCTTGAAGGGGACCGCAATGGAGGAGCAAAGAAGAAGAACTTTTTTAAACT
GAACAATAAAAGTGAAAAAGATAAGAAGGAAAAGAAACCAACTGTCAGTGTATTTTCAAT
GTTTCGCTATTCAAATTGGCTTGACAAGTTGTATATGGTGGTGGGAACTTTGGCTGCCAT
CATCCATGGGGCTGGACTTCCTCTCATGATGCTGGTGTTTGGAGAAATGACAGATATCTT
TGCAAATGCAGGAAATTTAGAAGATCTGATGTCAAACATCACTAATAGAAGTGATATCAA
TGATACAGGGTTCTTCATGAATCTGGAGGAAGACATGACCAGGTATGCCTATTATTACAG
TGGAATTGGTGCTGGGGTGCTGGTTGCTGCTTACATTCAGGTTTCATTTTGGTGCCTGGC
AGCTGGAAGACAAATACACAAAATTAGAAAACAGTTTTTTCATGCTATAATGCGACAGGA
GATAGGCTGGTTTGATGTGCACGATGTTGGGGAGCTTAACACCCGACTTACAGATGATGT
CTCTAAGATTAATGAAGTTATTGGTGACAAAATTGGAATGTTCTTTCAGTCAATGGCAAC
ATTTTTCACTGGGTTTATAGTAGGATTTACACGTGGTTGGAAGCTAACCCTTGTGATTTT
GGCCATCAGTCCTGTTCTTGGACTGTCAGCTGCTGTCTGGGCAAAGATACTATCTTCATT
TACTGATAAAGAACTCTTAGCGTATGCAAAAGCTGGAGCAGTAGCTGAAGAGGTCTTGGC
AGCAATTAGAACTGTGATTGCATTTGGAGGACAAAAGAAAGAACTTGAAAGGTACAACAA
AAATTTAGAAGAAGCTAAAAGAATTGGGATAAAGAAAGCTATTACAGCCAATATTTCTAT
AGGTGCTGCTTTCCTGCTGATCTATGCATCTTATGCTCTGGCCTTCTGGTATGGGACCAC
CTTGGTCCTCTCAGGGGAATATTCTATTGGACAAGTACTCACTGTATTCTTTTCTGTATT
AATTGGGGCTTTTAGTGTTGGACAGGCATCTCCAAGCATTGAAGCATTTGCAAATGCAAG
AGGAGCAGCTTATGAAATCTTCAAGATAATTGATAATAAGCCAAGTATTGACAGCTATTC
GAAGAGTGGGCACAAACCAGATAATATTAAGGGAAATTTGGAATTCAGAAATGTTCACTT
CAGTTACCCATCTCGAAAAGAAGTTAAGATCTTGAAGGGCCTGAACCTGAAGGTGCAGAG
TGGGCAGACGGTGGCCCTGGTTGGAAACAGTGGCTGTGGGAAGAGCACAACAGTCCAGCT
GATGCAGAGGCTCTATGACCCCACAGAGGGGATGGTCAGTGTTGATGGACAGGATATTAG
GACCATAAATGTAAGGTTTCTACGGGAAATCATTGGTGTGGTGAGTCAGGAACCTGTATT
GTTTGCCACCACGATAGCTGAAAACATTCGCTATGGCCGTGAAAATGTCACCATGGATGA
GATTGAGAAAGCTGTCAAGGAAGCCAATGCCTATGACTTTATCATGAAACTGCCTCATAA
ATTTGACACCCTGGTTGGAGAGAGAGGGGCCCAGTTGAGTGGTGGGCAGAAGCAGAGGAT

CGCCATTGCACGTGCCCTGGTTCGCAACCCCAAGATCCTCCTGCTGGATGAGGCCACGTC
AGCCTTGGACACAGAAAGCGAAGCAGTGGTTCAGGTGGCTCTGGATAAGGCCAGAAAAGG
TCGGACCACCATTGTGATAGCTCATCGTTTGTCTACAGTTCGTAATGCTGACGTCATCGC
TGGTTTCGATGATGGAGTCATTGTGGAGAAAGGAAATCATGATGAACTCATGAAAGAGAA
AGGCATTTACTTCAAACTTGTCACAATGCAGACAGCAGGAAATGAAGTTGAATTAGAAAA
TGCAGCTGATGAATCCAAAAGTGAAATTGATGCCTTGGAAATGTCTTCAAATGATTCAAG
ATCCAGTCTAATAAGAAAAAGATCAACTCGTAGGAGTGTCCGTGGATCACAAGCCCAAGA
CAGAAAGCTTAGTACCAAAGAGGCTCTGGATGAAAGTATACCTCCAGTTTCCTTTTGGAG
GATTATGAAGCTAAATTTAACTGAATGGCCTTATTTTGTTGTTGGTGTATTTTGTGCCAT
TATAAATGGAGGCCTGCAACCAGCATTTGCAATAATATTTTCAAAGATTATAGGGGTTTT
TACAAGAATTGATGATCCTGAAACAAAACGACAGAATAGTAACTTGTTTTCACTATTGTT
TCTAGCCCTTGGAATTATTTCTTTTATTACATTTTTCCTTCAGGGTTTCACATTTGGCAA
AGCTGGAGAGATCCTCACCAAGCGGCTCCGATACATGGTTTTCCGATCCATGCTCAGACA
GGATGTGAGTTGGTTTGATGACCCTAAAAACACCACTGGAGCATTGACTACCAGGCTCGC
CAATGATGCTGCTCAAGTTAAAGGGGCTATAGGTTCCAGGCTTGCTGTAATTACCCAGAA
TATAGCAAATCTTGGGACAGGAATAATTATATCCTTCATCTATGGTTGGCAACTAACACT
GTTACTCTTAGCAATTGTACCCATCATTGCAATAGCAGGAGTTGTTGAAATGAAAATGTT
GTCTGGACAAGCACTGAAAGATAAGAAAGAACTAGAAGGTGCTGGGAAGATCGCTACTGA
AGCAATAGAAAACTTCCGAACCGTTGTTTCTTTGACTCAGGAGCAGAAGTTTGAACATAT
GTATGCTCAGAGTTTGCAGGTACCATACAGAAACTCTTTGAGGAAAGCACACATCTTTGG
AATTACATTTTCCTTCACCCAGGCAATGATGTATTTTTCCTATGCTGGATGTTTCCGGTT
TGGAGCCTACTTGGTGGCACATAAACTCATGAGCTTTGAGGATGTTCTGTTAGTATTTTC
AGCTGTTGTCTTTGGTGCCATGGCCGTGGGGCAAGTCAGTTCATTTGCTCCTGACTATGC
CAAAGCCAAAATATCAGCAGCCCACATCATCATGATCATTGAAAAAACCCCTTTGATTGA
CAGCTACAGCACGGAAGGCCTAATGCCGAACACATTGGAAGGAAATGTCACATTTGGTGA
AGTTGTATTCAACTATCCCACCCGACCGGACATCCCAGTGCTTCAGGGACTGAGCCTGGA
GGTGAAGAAGGGCCAGACGCTGGCTCTGGTGGGCAGCAGTGGCTGTGGGAAGAGCACAGT
GGTCCAGCTCCTGGAGCGGTTCTACGACCCCTTGGCAGGGAAAGTGCTGCTTGATGGCAA
AGAAATAAAGCGACTGAATGTTCAGTGGCTCCGAGCACACCTGGGCATCGTGTCCCAGGA
GCCCATCCTGTTTGACTGCAGCATTGCTGAGAACATTGCCTATGGAGACAACAGCCGGGT
GGTGTCACAGGAAGAGATCGTGAGGGCAGCAAAGGAGGCCAACATACATGCCTTCATCGA
GTCACTGCCTAATAAATATAGCACTAAAGTAGGAGACAAAGGAACTCAGCTCTCTGGTGG
CCAGAAACAACGCATTGCCATAGCTCGTGCCCTTGTTAGACAGCCTCATATTTTGCTTTT
GGATGAAGCCACGTCAGCTCTGGATACAGAAAGTGAAAAGGTTGTCCAAGAAGCCCTGGA
CAAAGCCAGAGAAGGCCGCACCTGCATTGTGATTGCTCACCGCCTGTCCACCATCCAGAA
TGCAGACTTAATAGTGGTGTTTCAGAATGGCAGAGTCAAGGAGCATGGCACGCATCAGCA
GCTGCTGGCACAGAAAGGCATCTATTTTTCAATGGTCAGTGTCCAGGCTGGAACAAAGCG
CCAGTGAACTCTGACTGTATGAGATGTTAAATACTTTTTAATATTTGTTTAGATATGACA
TTTATTCAAAGTTAAAAGCAAACACTTACAGAATTATGAAGAGGTATCTGTTTAACATTT

SUBSTITUTE SHEET (RULE 26)

CCTCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAAGGAACAGAGTGAGAGACAT
CATCAAGTGGAGAGAAATCATAGTTTAAACTGCATTATAAATTTTATAACAGAATTAAAG
TAGATTTTAAAAGATAAAATGTGTAATTTTGTTTATATTTTCCCATTTGGACTGTAACTG
ACTGCCTTGCTAAAAGATTATAGAAGTAGCAAAAAGTATTGAAATGTTTGCATAAAGTGT
CTATAATAAAACTAAACTTTCATGTG

ABCB4 Acc. Nr.: M23234 GENBANK:HUMMDR3

CCTGCCAGACACGCGCGAGGTTCGAGGCTGAGATGGATCTTGAGGCGGCAAAGAACGGAA
CAGCCTGGCGCCCCACGAGCGCGGAGGGCGACTTTGAACTGGGCATCAGCAGCAAACAAA
AAAGGAAAAAAACGAAGACAGTGAAAATGATTGGAGTATTAACATTGTTTCGATACTCCG
ATTGGCAGGATAAATTGTTTATGTCGCTGGGTACCATCATGGCCATAGCTCACGGATCAG
GTCTCCCCCTCATGATGATAGTATTTGGAGAGATGACTGACAAATTTGTTGATACTGCAG
GAAACTTCTCCTTTCCAGTGAACTTTTCCTTGTCGCTGCTAAATCCAGGCAAAATTCTGG
AAGAAGAAATGACTAGATATGCATATTACTACTCAGGATTGGGTGCTGGAGTTCTTGTTG
CTGCCTATATACAAGTTTCATTTTGGACTTTGGCAGCTGGTCGACAGATCAGGAAAATTA
GGCAGAAGTTTTTTCATGCTATTCTACGACAGGAAATAGGATGGTTTGACATCAATGACA
CCACTGAACTCAATACGCGGCTAACAGATGACATCTCCAAAATCAGTGAAGGAATTGGTG
ACAAGGTTGGAATGTTCTTTCAAGCAGTAGCCACGTTTTTTGCAGGATTCATAGTGGGAT
TCATCAGAGGATGGAAGCTCACCCTTGTGATAATGGCCATCAGCCCTATTCTAGGACTCT
CTGCAGCCGTTTGGGCAAAGATACTCTCGGCATTTAGTGACAAAGAACTAGCTGCTTATG
CAAAAGCAGGCGCCGTGGCAGAAGAGGCTCTGGGGGCCATCAGGACTGTGATAGCTTTCG
GGGGCCAGAACAAAGAGCTGGAAAGGTATCAGAAACATTTAGAAAATGCCAAAGAGATTG
GAATTAAAAAAGCTATTTCAGCAAACATTTCCATGGGTATTGCCTTCCTGTTAATATATG
CATCATATGCACTGGCCTTCTGGTATGGATCCACTCTAGTCATATCAAAAGAATATACTA
TTGGAAATGCAATGACAGTTTTTTTTTCAATCCTAATTGGAGCTTTCAGTGTTGGCCAGG
CTGCCCCATGTATTGATGCTTTTGCCAATGCAAGAGGAGCAGCATATGTGATCTTTGATA
TTATTGATAATAATCCTAAAATTGACAGTTTTTCAGAGAGAGGACACAAACCAGACAGCA
TCAAAGGGAATTTGGAGTTCAATGATGTTCACTTTTCTTACCCTTCTCGAGCTAACGTCA
AGATCTTGAAGGGCCTCAACCTGAAGGTGCAGAGTGGGCAGACGGTGGCCCTGGTTGGAA
GTAGTGGCTGTGGGAAGAGCACAACGGTCCAGCTGATACAGAGGCTCTATGACCCTGATG
AGGGCACAATTAACATTGATGGGCAGGATATTAGGAACTTTAATGTAAACTATCTGAGGG
AAATCATTGGTGTGGTGAGTCAGGAGCCGGTGCTGTTTTCCACCACAATTGCTGAAAATA
TTTGTTATGGCCGTGGAAATGTAACCATGGATGAGATAAAGAAAGCTGTCAAAGAGGCCA
ACGCCTATGAGTTTATCATGAAATTACCACAGAAATTTGACACCCTGGTTGGAGAGAGAG
GGGCCCAGCTGAGTGGTGGGCAGAAGCAGAGGATCGCCATTGCACGTGCCCTGGTTCGCA
ACCCCAAGATCCTTCTGCTGGATGAGGCCACGTCAGCATTGGACACAGAAAGTGAAGCTG
AGGTACAGGCAGCTCTGGATAAGGCCAGAGAAGGCCGGACCACCATTGTGATAGCACACC
GACTGTCTACGGTCCGAAATGCAGATGTCATCGCTGGGTTTGAGGATGGAGTAATTGTGG
AGCAAGGAAGCCACAGCGAACTGATGAAGAAGGAAGGGGTGTACTTCAAACTTGTCAACA
TGCAGACATCAGGAAGCCAGATCCAGTCAGAAGAATTTGAACTAAATGATGAAAAGGCTG

CCACTAGAATGGCCCCAAATGGCTGGAAATCTCGCCTATTTAGGCATTCTACTCAGAAAA
ACCTTAAAAATTCACAAATGTGTCAGAAGAGCCTTGATGTGGAAACCGATGGACTTGAAG
CAAATGTGCCACCAGTGTCCTTTCTGAAGGTCCTGAAACTGAATAAAACAGAATGGCCCT
ACTTTGTCGTGGGAACAGTATGTGCCATTGCCAATGGGGGGCTTCAGCCGGCATTTTCAG
TCATATTCTCAGAGATCATAGCGATTTTTGGACCAGGCGATGATGCAGTGAAGCAGCAGA
AGTGCAACATATTCTCTTTGATTTTCTTATTTCTGGGAATTATTTCTTTTTTTACTTTCT
TCCTTCAGGGTTTCACGTTTGGGAAAGCTGGCGAGATCCTCACCAGAAGACTGCGGTCAA
TGGCTTTTAAAGCAATGCTAAGACAGGACATGAGCTGGTTTGATGACCATAAAAACAGTA
CTGGTGCACTTTCTACAAGACTTGCCACAGATGCTGCCCAAGTCCAAGGAGCCACAGGAA
CCAGGTTGGCTTTAATTGCACAGAATATAGCTAACCTTGGAACTGGTATTATCATATCAT
TTATCTACGGTTGGCAGTTAACCCTATTGCTATTAGCAGTTGTTCCAATTATTGCTGTGT
CAGGAATTGTTGAAATGAAATTGTTGGCTGGAAATGCCAAAAGAGATAAAAAAGAACTGG
AAGCTGCTGGAAAGATTGCAACAGAGGCAATAGAAAATATTAGGACAGTTGTGTCTTTGA
CCCAGGAAAGAAAATTTGAATCAATGTATGTTGAAAAATTGTATGGACCTTACAGGAATT
CTGTGCAGAAGGCACACATCTATGGAATTACTTTTAGTATCTCACAAGCATTTATGTATT
TTTCCTATGCCGGTTGTTTTCGATTTGGTGCATATCTCATTGTGAATGGACATATGCGCT
TCAGAGATGTTATTCTGGTGTTTTCTGCAATTGTATTTGGTGCAGTGGCTCTAGGACATG
CCAGTTCATTTGCTCCAGACTATGCTAAAGCTAAGCTGTCTGCAGCCCACTTATTCATGC
TGTTTGAAAGACAACCTCTGATTGACAGCTACAGTGAAGAGGGGCTGAAGCCTGATAAAT
TTGAAGGAAATATAACATTTAATGAAGTCGTGTTCAACTATCCCACCCGAGCAAACGTGC
CAGTGCTTCAGGGGCTGAGCCTGGAGGTGAAGAAAGGCCAGACACTAGCCCTGGTGGGCA
GCAGTGGCTGTGGGAAGAGCACGGTGGTCCAGCTCCTGGAGCGGTTCTACGACCCCTTGG
CGGGGACAGTGCTTCTCGATGGTCAAGAAGCAAAGAAACTCAATGTCCAGTGGCTCAGAG
CTCAACTCGGAATCGTGTCTCAGGAGCCTATCCTATTTGACTGCAGCATTGCCGAGAATA
TTGCCTATGGAGACAACAGCCGGGTTGTATCACAGGATGAAATTGTGAGTGCAGCCAAAG
CTGCCAACATACATCCTTTCATCGAGACGTTACCCCACAAATATGAAACAAGAGTGGGAG
ATAAGGGGACTCAGCTCTCAGGAGGTCAAAAACAGAGGATTGCTATTGCCCGAGCCCTCA
TCAGACAACCTCAAATCCTCCTGTTGGATGAAGCTACATCAGCTCTGGATACTGAAAGTG
AAAAGGTTGTCCAAGAAGCCCTGGACAAAGCCAGAGAAGGCCGCACCTGCATTGTGATTG
CTCACCGCCTGTCCACCATCCAGAATGCAGACTTAATAGTGGTGTTTCAGAATGGGAGAG
TCAAGGAGCATGGCACGCATCAGCAGCTGCTGGCACAGAAAGGCATCTATTTTTCAATGG
TCAGTGTCCAGGCTGGGACACAGAACTTATGAACTTTTGCTACAGTATATTTTAAAAATA
AATTCAAATTATTCTACCCATTTT

ABCC2 Acc.Nr.: U49248 GENBANK:HSU49248

AGGATAATTCCTGTTCCACTTTCTTTGATGAAACAAGTAAAGAAGAAACAACACAATCAT
ATTAATAGAAGAGTCTTCGTTCCAGACGCAGTCCAGGAATCATGCTGGAGAAGTTCTGCA
ACTCTACTTTTTGGAATTCCTCATTCCTGGACAGTCCGGAGGCAGACCTGCCACTTTGTT
TTGAGCAAACTGTTCTGGTGTGGATTCCCTTGGGCTTCCTATGGCTCCTGGCCCCCTGGC
AGCTTCTCCACGTGTATAAATCCAGGACCAAGAGATCCTCTACCACCAAACTCTATCTTG

GAAGATGCTGAAACCTTCTATGACAACTCTACAACTCCTTACTGCAATGATTTGATGAAG
AATTTGGAGTCTAGTCCTCTTTCCCGCATTATCTGGAAAGCTCTGAAGCCGCTGCTCGTT
GGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGGCAGGTCATGGCTGAGGTGAAC
AAGACCTTCCAGGAACTGGCTGTGTTCCATGATCTGGAAGGCATGTGGGAGGAACTCAGC
CCCAAGATCTGGACCTTCATGGAGAACAGCCAAGAAATGGACCTTGTCCGGATGCTGTTG
GACAGCAGGGACAATGACCACTTTTGGGAACAGCAGTTGGATGGCTTAGATTGGACAGCC
CAAGACATCGTGGCGTTTTTGGCCAAGCACCCAGAGGATGTCCAGTCCAGTAATGGTTCT
GTGTACACCTGGAGAGAAGCTTTCAACGAGACTAACCAGGCAATCCGGACCATATCTCGC
TTCATGGAGTGTGTCAACCTGAACAAGCTAGAACCCATAGCAACAGAAGTCTGGCTCATC
AACAAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTATTGTGTTCACTGGA
ATTACTCCAGGCAGCATTGAGCTGCCCCATCATGTCAAGTACAAGATCCGAATGGACATT
GACAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACCCTGGTCCTCGAGCT
GACCCCTTTGAGGACATGCGGTACGTCTGGGGGGGCTTCGCCTACTTGCAGGATGTGGTG
GAGCAGGCAATCATCAGGGTGCTGACGGGCACCGAGAAGAAAACTGGTGTCTATATGCAA
CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGCGGGTGATGAGCCGGTCAATG
CCCCTCTTCATGACGCTGGCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG
TATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACAGCATC
CTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTCTTGTGAGCGCTGGCCTGCTA
GTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTTTGTC
TTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACACTCTTC
TCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCC
TACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC
CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTTGAGGAGCAG
GGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCTGTGGAGGAAGATGGCTTCAAT
CTCACCACTTCGGTCTCCATGATGCTGTTTGACACCTTCCTCTATGGGGTGATGACCTGG
TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATTCCCAGGCCCTGGTATTTTCCTTGC
ACCAAGTCCTACTGGTTTGGCGAGGAAAGTGATGAGAAGAGCCACCCTGGTTCCAACCAG
AAGAGAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGAAGCTGGGCGTGTCC
ATTCAGAACCTGGTAAAAGTCTACCGAGATGGGATGAAGGTGGCTGTCGATGGCCTGGCA
CTGAATTTTTATGAGGGCCAGATCACCTCCTTCCTGGGCCACAATGGAGCGGGGAAGACG
ACCACCATGTCAATCCTGACCGGGTTGTTCCCCCCGACCTCGGGCACCGCCTACATCCTG
GGAAAAGACATTCGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGGTCTGTCCCCAG
CATAACGTGCTGTTTGACATGCTGACTGTCGAAGAACACATCTGGTTCTATGCCCGCTTG
AAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT
TTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTCAGGTGGAATGCAGAGAAAG
CTATCTGTGGCCTTGGCCTTTGTCGGGGGATCTAAGGTTGTCATTCTGGATGAACCCACA
GCTGGTGTGGACCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA
GGCCGCACCATTATTCTCTCTACACACCACATGGATGAAGCGGACGTCCTGGGGGACAGG
ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCCTGTTTCTGAAGAAC

SUBSTITUTE SHEET (RULE 26)

CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT
TCCTGCAGAAACAGTAGTAGCACTGTGTCATACCTGAAAAAGGAGGACAGTGTTTCTCAG
AGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAGAGTGACACGCTGACCATCGATGTC
TCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCGGCTGGTGGAAGACATA
GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGGAGCCTTTGTGGAA
CTCTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA
GAGACGACCCTGGAAGAAATATTCCTCAAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAG
ACCTCAGATGGTACCTTGCCAGCAAGACGAAACAGGCGGGCCTTCGGGGACAAGCAGAGC
TGTCTTCGCCCGTTCACTGAAGATGATGCTGCTGATCCAAATGATTCTGACATAGACCCA
GAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGGTCCTACCAGGTGAAA
GGCTGGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAATTGCC
AGACGGAGTCGGAAAGGATTTTTTGCTCAGATTGTCTTGCCAGCTGTGTTTGTCTGCATT
GCCCTTGTGTTCAGCCTGATCGTGCCACCCTTTGGCAAGTACCCCAGCCTGGAACTTCAG
CCCTGGATGTACAACGAACAGTACACATTTGTCAGCAATGATGCTCCTGAGGACACGGGA
ACCCTGGAACTCTTAAACGCCCTCACCAAAGACCCTGGCTTCGGGACCCGCTGTATGGAA
GGAAACCCAATCCCAGACACGCCCTGCCAGGCAGGGGAGGAAGAGTGGACCACTGCCCCA
GTTCCCCAGACCATCATGGACCTCTTCCAGAATGGGAACTGGACAATGCAGAACCCTTCA
CCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTGTGTGTCCCCCAGGG
GCAGGGGGGCTGCCTCCTCCACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTG
ACAGGAAGAAACATTTCGGATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGC
TTAAAGAACAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGT
AATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAA
CACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTT
ATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCAT
GCAATCAGCTCTTTCCTGAATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAG
GGAGAGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAG
CAGCAGCTCTCAGAGGTGGCTCCGATGACCACATCAGTGGATGTCCTTGTGTCCATCTGT
GTCATCTTTGCAATGTCCTTCGTCCCAGCCAGCTTTGTCGTATTCCTGATCCAGGAGCGG
GTCAGCAAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTGTCATCTACTGGCTC
TCTAATTTTGTCTGGGATATGTGCAATTACGTTGTCCCTGCCACACTGGTCATTATCATC
TTCATCTGCTTCCAGCAGAAGTCCTATGTGTCCTCCACCAATCTGCCTGTGCTAGCCCTT
CTACTTTTGCTGTATGGGTGGTCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGTTC
AAGATCCCCAGCACAGCCTATGTGGTGCTCACCAGCGTGAACCTCTTCATTGGCATTAAT
GGCAGCGTGGCCACCTTTGTGCTGGAGCTGTTCACCGACAATAAGCTGAATAATATCAAT
GATATCCTGAAGTCCGTGTTCTTGATCTTCCCACATTTTTGCCTGGGACGAGGGCTCATC
GACATGGTGAAAAACCAGGCAATGGCTGATGCCCTGGAAAGGTTTGGGGAGAATCGCTTT
GTGTCACCATTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGG
GTGGTGTTCTTCCTCATTACTGTTCTGATCCAGTACAGATTCTTCATCAGGCCCAGACCT
GTAAATGCAAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGAGGCGGGAAAGACAG

CTAAGCAGGTATTCGTTGGTTTTCTTCTTATTCTAGCAGCCATAGAGCTGGCCCTTGTAC
TCACAGAAGACTCTGGACAAGCCACAGTCCCTGCTGTTCGATATACCAATCCAAGCCTCT
ACCTAGGCACATGGCTCCTGGTTTTGCTGATCCAATACAGCAGACAATGGTGTGTACAGA
AAAACTCCTGGTTCCTGTCCCTATTCTGGATTCTCTCGATACTCTGTGGCACTTTCCAAT
TTCAGACTCTGATCCGGACACTCTTACAGGGTGACAATTCTAATCTAGCCTACTCCTGCC
TGTTCTTCATCTCCTACGGATTCCAGATCCTGATCCTGATCTTTTCAGCATTTTCAGAAA
ATAATGAGTCATCAAATAATCCATCATCCATAGCTTCATTCCTGAGTAGCATTACCTACA
GCTGGTATGACAGCATCATTCTGAAAGGCTACAAGCGTCCTCTGACACTCGAGGATGTCT
GGGAAGTTGATGAAGAGATGAAAACCAAGACATTAGTGAGCAAGTTTGAAACGCACATGA
AGAGAGAGCTGCAGAAAGCCAGGCGGGCACTCCAGAGACGGCAGGAGAAGAGCTCCCAGC
AGAACTCTGGAGCCAGGCTGCCTGGCTTGAACAAGAATCAGAGTCAAAGCCAAGATGCCC
TTGTCCTGGAAGATGTTGAAAAGAAAAAAAAGAAGTCTGGGACCAAAAAAGATGTTCCAA
AATCCTGGTTGATGAAGGCTCTGTTCAAAACTTTCTACATGGTGCTCCTGAAATCATTCC
TACTGAAGCTAGTGAATGACATCTTCACGTTTGTGAGTCCTCAGCTGCTGAAATTGCTGA
TCTCCTTTGCAAGTGACCGTGACACATATTTGTGGATTGGATATCTCTGTGCAATCCTCT
TATTCACTGCGGCTCTCATTCAGTCTTTCTGCCTTCAGTGTTATTTCCAACTGTGCTTCA
AGCTGGGTGTAAAAGTACGGACAGCTATCATGGCTTCTGTATATAAGAAGGCATTGACCC
TATCCAACTTGGCCAGGAAGGAGTACACCGTTGGAGAAACAGTGAACCTGATGTCTGTGG
ATGCCCAGAAGCTCATGGATGTGACCAACTTCATGCACATGCTGTGGTCAAGTGTTCTAC
AGATTGTCTTATCTATCTTCTTCCTATGGAGAGAGTTGGGACCCTCAGTCTTAGCAGGTG
TTGGGGTGATGGTGCTTGTAATCCCAATTAATGCGATACTGTCCACCAAGAGTAAGACCA
TTCAGGTCAAAAATATGAAGAATAAAGACAAACGTTTAAAGATCATGAATGAGATTCTTA
GTGGAATCAAGATCCTGAAATATTTTGCCTGGGAACCTTCATTCAGAGACCAAGTACAAA
ACCTCCGGAAGAAAGAGCTCAAGAACCTGCTGGCCTTTAGTCAACTACAGTGTGTAGTAA
TATTCGTCTTCCAGTTAACTCCAGTCCTGGTATCTGTGGTCACATTTTCTGTTTATGTCC
TGGTGGATAGCAACAATATTTTGGATGCACAAAAGGCCTTCACCTCCATTACCCTCTTCA
ATATCCTGCGCTTTCCCCTGAGCATGCTTCCCATGATGATCTCCTCCATGCTCCAGGCCA
GTGTTTCCACAGAGCGGCTAGAGAAGTACTTGGGAGGGGATGACTTGGACACATCTGCCA
TTCGACATGACTGCAATTTTGACAAAGCCATGCAGTTTTCTGAGGCCTCCTTTACCTGGG
AACATGATTCGGAAGCCACAGTCCGAGATGTGAACCTGGACATTATGGCAGGCCAACTTG
TGGCTGTGATAGGCCCTGTCGGCTCTGGGAAATCCTCCTTGATATCAGCCATGCTGGGAG
AAATGGAAAATGTCCACGGGCACATCACCATCAAGGGCACCACTGCCTATGTCCCACAGC
AGTCCTGGATTCAGAATGGCACCATAAAGGACAACATCCTTTTTGGAACAGAGTTTAATG
AAAAGAGGTACCAGCAAGTACTGGAGGCCTGTGCTCTCCTCCCAGACTTGGAAATGCTGC
CTGGAGGAGATTTGGCTGAGATTGGAGAGAAGGGTATAAATCTTAGTGGGGGTCAGAAGC
AGCGGATCAGCCTGGCCAGAGCTACCTACCAAAATTTAGACATCTATCTTCTAGATGACC
CCCTGTCTGCAGTGGATGCTCATGTAGGAAAACATATTTTTAATAAGGTCTTGGGCCCCA
ATGGCCTGTTGAAAGGCAAGACTCGACTCTTGGTTACACATAGCATGCACTTTCTTCCTC
AAGTGGATGAGATTGTAGTTCTGGGGAATGGAACAATTGTAGAGAAAGGATCCTACAGTG

SUBSTITUTE SHEET (RULE 26)

CTCTCCTGGCCAAAAAAGGAGAGTTTGCTAAGAATCTGAAGACATTTCTAAGACATACAG
GCCCTGAAGAGGAAGCCACAGTCCATGATGGCAGTGAAGAAGAAGACGATGACTATGGGC
TGATATCCAGTGTGGAAGAGATCCCCGAAGATGCAGCCTCCATAACCATGAGAAGAGAGA
ACAGCTTTCGTCGAACACTTAGCCGCAGTTCTAGGTCCAATGGCAGGCATCTGAAGTCCC
TGAGAAACTCCTTGAAAACTCGGAATGTGAATAGCCTGAAGGAAGACGAAGAACTAGTGA
AAGGACAAAAACTAATTAAGAAGGAATTCATAGAAACTGGAAAGGTGAAGTTCTCCATCT
ACCTGGAGTACCTACAAGCAATAGGATTGTTTTCGATATTCTTCATCATCCTTGCGTTTG
TGATGAATTCTGTGGCTTTTATTGGATCCAACCTCTGGCTCAGTGCTTGGACCAGTGACT
CTAAAATCTTCAATAGCACCGACTATCCAGCATCTCAGAGGGACATGAGAGTTGGAGTCT
ACGGAGCTCTGGGATTAGCCCAAGGTATATTTGTGTTCATAGCACATTTCTGGAGTGCCT
TTGGTTTCGTCCATGCATCAAATATCTTGCACAAGCAACTGCTGAACAATATCCTTCGAG
CACCTATGAGATTTTTTGACACAACACCCACAGGCCGGATTGTGAACAGGTTTGCCGGCG
ATATTTCCACAGTGGATGACACCCTGCCTCAGTCCTTGCGCAGCTGGATTACATGCTTCC
TGGGGATAATCAGCACCCTTGTCATGATCTGCATGGCCACTCCTGTCTTCACCATCATCG
TCATTCCTCTTGGCATTATTTATGTATCTGTTCAGATGTTTTATGTGTCTACCTCCCGCC
AGCTGAGGCGTCTGGACTCTGTCACCAGGTCCCCAATCTACTCTCACTTCAGCGAGACCG
TATCAGGTTTGCCAGTTATCCGTGCCTTTGAGCACCAGCAGCGATTTCTGAAACACAATG
AGGAGAGGATTGACACCAACCAGAAATGTGTCTTTTCCTGGATCACCTCCAACAGGTGGC
TTGCAATTCGCCTGGAGCTGGTTGGGAACCTGACTGTCTTCTTTTCAGCCTTGATGATGG
TTATTTATAGAGATACCCTAAGTGGGGACACTGTTGGCTTTGTTCTGTCCAATGCACTCA
ATATCACACAAACCCTGAACTGGCTGGTGAGGATGACATCAGAAATAGAGACCAACATTG
TGGCTGTTGAGCGAATAACTGAGTACACAAAAGTGGAAAATGAGGCACCCTGGGTGACTG
ATAAGAGGCCTCCGCCAGATTGGCCCAGCAAAGGCAAGATCCAGTTTAACAACTACCAAG
TGCGGTACCGACCTGAGCTGGATCTGGTCCTCAGAGGGATCACTTGTGACATCGGTAGCA
TGGAGAAGATTGGTGTGGTGGGCAGGACAGGAGCTGGAAAGTCATCCCTCACAAACTGCC
TCTTCAGAATCTTAGAGGCTGCCGGTGGTCAGATTATCATTGATGGAGTAGATATTGCTT
CCATTGGGCTCCACGACCTCCGAGAGAAGCTGACCATCATCCCCCAGGACCCCATCCTGT
TCTCTGGAAGCCTGAGGATGAATCTCGACCCTTTCAACAACTACTCAGATGAGGAGATTT
GGAAGGCCTTGGAGCTGGCTCACCTCAAGTCTTTTGTGGCCAGCCTGCAACTTGGGTTAT
CCCACGAAGTTACAGAGGCTGGTGGCAACCTGAGCATAGGCCAGAGGCAGCTGCTGTGCC
TGGGCAGGGCTCTGCTTCGGAAATCCAAGATCCTGGTCCTGGATGAGGCCACTGCTGCGG
TGGATCTAGAGACAGACAACCTCATTCAGACGACCATCCAAAACGAGTTCGCCCACTGCA
CAGTGATCACCATCGCCCACAGGCTGCATACCATCATGGACAGTGACAAGGTAATGGTCC
TAGACAACGGGAAGATTATAGAGTACGGCAGCCCTGAAGAACTGCTACAAATCCCTGGAC
CCTTTTACTTTATGGCTAAGGAAGCTGGCATTGAGAATGTGAACAGCACAAAATTCTAGC
AGAAGGCCCCATGGGTTAGAAAAGGACTATAAGAATAATTTCTTATTTAATTTTATTTTT
TATAAAATACAGAATACATACAAAAGTGTGTATAAAATGTACGTTTTAAAAAAGGATAAG
TGAACACCCATGAACCTACTACCCAGGTTAAGAAAATAAATGTCACCAGGTACTTGAGAA
ACCCCTCGATTGTCTACCTCGATCGTACTTCCTTGCTACCCACCCCTCCCAGGGACAACC

SUBSTITUTE SHEET (RULE 26)

ACTGTCCTGAATTTCACGATAATTATTCCTTTGCCTTTCATTTCTGTTTTATCACCTTTG
TATGTATCTTTAAACAACATATACCCTTTTTTACTTATGTAAATGGACTGACTCATACTG
CATACATCTTCTATGACTTGATTCTTTTGTTCAATATTATATCTGAGATTCATCCATGGT
GATGCAAATAGGTGCATTATTTTTTTTCACTGCTCTGTAGTCTGGCATTGTATGAATACA
GCACAATGTATCAGTTTTAATATTGGGGATCATTAGCATTATTCTCAGGTTTTTAAAAAT
TATAAGCAGTACTACTATGG

ABCD1 Acc.Nr.: Z21876 GENBANK:HSXLALDA

GCGGACGGACGCGCCTGGTGCCCCGGGGAGGGGCGCCACCGGGGGAGGAGGAGGAGGAGA
AGGTGGAGAGGAAGAGACGCCCCCTCTGCCCGAGACCTCTCAAGGCCCTGACCTCAGGGG
CCAGGGCACTGACAGGACAGGAGAGCCAAGTTCCTCCACTTGGGCTGCCCGAAGAGGCCG
CGACCCTGGAGGGCCCTGAGCCCACCGCACCAGGGGCCCCAGCACCACCCCGGGGGCCTA
AAGCGACAGTCTCAGGGGCCATCGCAAGGTTTCCAGTTGCCTAGACAACAGGCCCAGGGT
CAGAGCAACAATCCTTCCAGCCACCTGCCTCAACTGCTGCCCCAGGCACCAGCCCCAGTC
CCTACGCGGCAGCCAGCCCAGGTGACATGCCGGTGCTCTCCAGGCCCCGGCCCTGGCGGG
GGAACACGCTGAAGCGCACGGCCGTGCTCCTGGCCCTCGCGGCCTATGGAGCCCACAAAG
TCTACCCCTTGGTGCGCCAGTGCCTGGCCCCGGCCAGGGGTCTTCAGGCGCCCGCCGGGG
AGCCCACGCAGGAGGCCTCCGGGGTCGCGGCGGCCAAAGCTGGCATGAACCGGGTATTCC
TGCAGCGGCTCCTGTGGCTCCTGCGGCTGCTGTTCCCCCGGGTCCTGTGCCGGGAGACGG
GGCTGCTGGCCCTGCACTCGGCCGCCTTGGTGAGCCGCACCTTCCTGTCGGTGTATGTGG
CCCGCCTGGACGGAAGGCTGGCCCGCTGCATCGCCCGCAAGGACCCGCGGGCTTTTGGCT
GGCAGCTGCTGCAGTGGCTCCTCATCGCCCTCCCTGCTACCTTCGTCAACAGTGCCATCC
GTTACCTGGAGGGCCAACTGGCCCTGTCGTTCCGCAGCCGTCTGGTGGCCCACGCCTACC
GCCTCTACTTCTCCCAGCAGACCTACTACCGGGTCAGCAACATGGACGGGCGGCTTCGCA
ACCCTGACCAGTCTCTGACGGAGGACGTGGTGGCCTTTGCGGCCTCTGTGGCCCACCTCT
ACTCCAACCTGACCAAGCCACTCCTGGACGTGGCTGTGACTTCCTACACCCTGCTTCGGG
CGGCCCGCTCCCGTGGAGCCGGCACAGCCTGGCCCTCGGCCATCGCCGGCCTCGTGGTGT
TCCTCACGGCCAACGTGCTGCGGGCCTTCTCGCCCAAGTTCGGGGAGCTGGTGGCAGAGG
AGGCGCGGCGGAAGGGGGAGCTGCGCTACATGCACTCGCGTGTGGTGGCCAACTCGGAGG
AGATCGCCTTCTATGGGGGCCATGAGGTGGAGCTGGCCCTGCTACAGCGCTCCTACCAGG
ACCTGGCCTCGCAGATCAACCTCATCCTTCTGGAACGCCTGTGGTATGTTATGCTGGAGC
AGTTCCTCATGAAGTATGTGTGGAGCGCCTCGGGCCTGCTCATGGTGGCTGTCCCCATCA
TCACTGCCACTGGCTACTCAGAGTCAGATGCAGAGGCCGTGAAGAAGGCAGCCTTGGAAA
AGAAGGAGGAGGAGCTGGTGAGCGAGCGCACAGAAGCCTTCACTATTGCCCGCAACCTCC
TGACAGCGGCTGCAGATGCCATTGAGCGGATCATGTCGTCGTACAAGGAGGTGACGGAGC
TGGCTGGCTACACAGCCCGGGTGCACGAGATGTTCCAGGTATTTGAAGATGTTCAGCGCT
GTCACTTCAAGAGGCCCAGGGAGCTAGAGGACGCTCAGGCGGGGTCTGGGACCATAGGCC
GGTCTGGTGTCCGTGTGGAGGGCCCCCTGAAGATCCGAGGCCAGGTGGTGGATGTGGAAC
AGGGGATCATCTGCGAGAACATCCCCATCGTCACGCCCTCAGGAGAGGTGGTGGTGGCCA
GCCTCAACATCAGGGTGGAGGAAGGCATGCATCTGCTCATCACAGGCCCCAATGGCTGCG

SUBSTITUTE SHEET (RULE 26)

GCAAGAGCTCCCTGTTCCGGATCCTGGGTGGGCTCTGGCCCACGTACGGTGGTGTGCTCT
ACAAGCCCCCACCCCAGCGCATGTTCTACATCCCGCAGAGGCCCTACATGTCTGTGGGCT
CCCTGCGTGACCAGGTGATCTACCCGGACTCAGTGGAGGACATGCAAAGGAAGGGCTACT
CGGAGCAGGACCTGGAAGCCATCCTGGACGTCGTGCACCTGCACCACATCCTGCAGCGGG
AGGGAGGTTGGGAGGCTATGTGTGACTGGAAGGACGTCCTGTCGGGTGGCGAGAAGCAGA
GAATCGGCATGGCCCGCATGTTCTACCACAGGCCCAAGTACGCCCTCCTGGATGAATGCA
CCAGCGCCGTGAGCATCGACGTGGAAGGCAAGATCTTCCAGGCGGCCAAGGACGCGGGCA
TTGCCCTGCTCTCCATCACCCACCGGCCCTCCCTGTGGAAATACCACACACACTTGCTAC
AGTTCGATGGGGAGGGCGGCTGGAAGTTCGAGAAGCTGGACTCAGCTGCCCGCCTGAGCC
TGACGGAGGAGAAGCAGCGGCTGGAGCAGCAGCTGGCGGGCATTCCCAAGATGCAGCGGC
GCCTCCAGGAGCTCTGCCAGATCCTGGGCGAGGCCGTGGCCCCAGCGCATGTGCCGGCAC
CTAGCCCGCAAGGCCCTGGTGGCCTCCAGGGTGCCTCCACCTGACACAACCGTCCCCGGC
CCCTGCCCCGCCCCCAAGCTCGGATCACATGAAGGAGACAGCAGCACCCACCCATGCACG
CACCCCGCCCCTGCATGCCTGGCCCCTCCTCCTAGAAAACCCTTCCCGCC

ABCC1 Acc.Nr.: L05628 GENBANK:HUMMRPX

CCAGGCGGCGTTGCGGCCCCGGCCCCGGCTCCCTGCGCCGCCGCCGCCGCCGCCGCCGCC
GCCGCCGCCGCCGCCGCCAGCGCTAGCGCCAGCAGCCGGGCCCGATCACCCGCCGCCCGG
TGCCCGCCGCCGCCCGCGCCAGCAACCGGGCCCGATCACCCGCCGCCCGGTGCCCGCCGC
CGCCCGCGCCACCGGCATGGCGCTCCGGGGCTTCTGCAGCGCCGATGGCTCCGACCCGCT
CTGGGACTGGAATGTCACGTGGAATACCAGCAACCCCGACTTCACCAAGTGCTTTCAGAA
CACGGTCCTCGTGTGGGTGCCTTGTTTTTACCTCTGGGCCTGTTTCCCCTTCTACTTCCT
CTATCTCTCCCGACATGACCGAGGCTACATTCAGATGACACCTCTCAACAAAACCAAAAC
TGCCTTGGGATTTTTGCTGTGGATCGTCTGCTGGGCAGACCTCTTCTACTCTTTCTGGGA
AAGAAGTCGGGGCATATTCCTGGCCCCAGTGTTTCTGGTCAGCCCAACTCTCTTGGGCAT
CACCACGCTGCTTGCTACCTTTTTAATTCAGCTGGAGAGGAGGAAGGGAGTTCAGTCTTC
AGGGATCATGCTCACTTTCTGGCTGGTAGCCCTAGTGTGTGCCCTAGCCATCCTGAGATC
CAAAATTATGACAGCCTTAAAAGAGGATGCCCAGGTGGACCTGTTTCGTGACATCACTTT
CTACGTCTACTTTTCCCTCTTACTCATTCAGCTCGTCTTGTCCTGTTTCTCAGATCGCTC
ACCCCTGTTCTCGGAAACCATCCACGACCCTAATCCCTGCCCAGAGTCCAGCGCTTCCTT
CCTGTCGAGGATCACCTTCTGGTGGATCACAGGGTTGATTGTCCGGGGCTACCGCCAGCC
CCTGGAGGGCAGTGACCTCTGGTCCTTAAACAAGGAGGACACGTCGGAACAAGTCGTGCC
TGTTTTGGTAAAGAACTGGAAGAAGGAATGCGCCAAGACTAGGAAGCAGCCGGTGAAGGT
TGTGTACTCCTCCAAGGATCCTGCCCAGCCGAAAGAGAGTTCCAAGGTGGATGCGAATGA
GGAGGTGGAGGCTTTGATCGTCAAGTCCCCACAGAAGGAGTGGAACCCCTCTCTGTTTAA
GGTGTTATACAAGACCTTTGGGCCCTACTTCCTCATGAGCTTCTTCTTCAAGGCCATCCA
CGACCTGATGATGTTTTCCGGGCCGCAGATCTTAAAGTTGCTCATCAAGTTCGTGAATGA
CACGAAGGCCCCAGACTGGCAGGGCTACTTCTACACCGTGCTGCTGTTTGTCACTGCCTG
CCTGCAGACCCTCGTGCTGCACCAGTACTTCCACATCTGCTTCGTCAGTGGCATGAGGAT
CAAGACCGCTGTCATTGGGGCTGTCTATCGGAAGGCCCTGGTGATCACCAATTCAGCCAG

AAAATCCTCCACGGTCGGGGAGATTGTCAACCTCATGTCTGTGGACGCTCAGAGGTTCAT
GGACTTGGCCACGTACATTAACATGATCTGGTCAGCCCCCCTGCAAGTCATCCTTGCTCT
CTACCTCCTGTGGCTGAATCTGGGCCCTTCCGTCCTGGCTGGAGTGGCGGTGATGGTCCT
CATGGTGCCCGTCAATGCTGTGATGGCGATGAAGACCAAGACGTATCAGGTGGCCCACAT
GAAGAGCAAAGACAATCGGATCAAGCTGATGAACGAAATTCTCAATGGGATCAAAGTGCT
AAAGCTTTATGCCTGGGAGCTGGCATTCAAGGACAAGGTGCTGGCCATCAGGCAGGAGGA
GCTGAAGGTGCTGAAGAAGTCTGCCTACCTGTCAGCCGTGGGCACCTTCACCTGGGTCTG
CACGCCCTTTCTGGTGGCCTTGTGCACATTTGCCGTCTACGTGACCATTGACGAGAACAA
CATCCTGGATGCCCAGACAGCCTTCGTGTCTTTGGCCTTGTTCAACATCCTCCGGTTTCC
CCTGAACATTCTCCCCATGGTCATCAGCAGCATCGTGCAGGCGAGTGTCTCCCTCAAACG
CCTGAGGATCTTTCTCTCCCATGAGGAGCTGGAACCTGACAGCATCGAGCGACGGCCTGT
CAAAGACGGCGGGGGCACGAACAGCATCACCGTGAGGAATGCCACATTCACCTGGGCCAG
GAGCGACCCTCCCACACTGAATGGCATCACCTTCTCCATCCCCGAAGGTGCTTTGGTGGC
CGTGGTGGGCCAGGTGGGCTGCGGAAAGTCGTCCCTGCTCTCAGCCCTCTTGGCTGAGAT
GGACAAAGTGGAGGGGCACGTGGCTATCAAGGGCTCCGTGGCCTATGTGCCACAGCAGGC
CTGGATTCAGAATGATTCTCTCCGAGAAAACATCCTTTTTGGATGTCAGCTGGAGGAACC
ATATTACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCCAGACCTGGAAATCCTGCCCAG
TGGGGATCGGACAGAGATTGGCGAGAAGGGCGTGAACCTGTCTGGGGGCCAGAAGCAGCG
CGTGAGCCTGGCCCGGGCCGTGTACTCCAACGCTGACATTTACCTCTTCGATGATCCCCT
CTCAGCAGTGGATGCCCATGTGGGAAAACACATCTTTGAAAATGTGATTGGCCCCAAGGG
GATGCTGAAGAACAAGACGCGGATCTTGGTCACGCACAGCATGAGCTACTTGCCGCAGGT
GGACGTCATCATCGTCATGAGTGGCGGCAAGATCTCTGAGATGGGCTCCTACCAGGAGCT
GCTGGCTCGAGACGGCGCCTTCGCTGAGTTCCTGCGTACCTATGCCAGCACAGAGCAGGA
GCAGGATGCAGAGGAGAACGGGGTCACGGGCGTCAGCGGTCCAGGGAAGGAAGCAAAGCA
AATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAGCAACTGCAGAGACAGCTCAG
CAGCTCCTCCTCCTATAGTGGGGACATCAGCAGGCACCACAACAGCACCGCAGAACTGCA
GAAAGCTGAGGCCAAGAAGGAGGAGACCTGGAAGCTGATGGAGGCTGACAAGGCGCAGAC
AGGGCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAGGCCATCGGACTCTTCATCTC
CTTCCTCAGCATCTTCCTTTTCATGTGTAACCATGTGTCCGCGCTGGCTTCCAACTATTG
GCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACTCAGGAGCACACGAAAGTCCG
GCTGAGCGTCTATGGAGCCCTGGGCATTTCACAAGGGATCGCCGTGTTTGGCTACTCCAT
GGCCGTGTCCATCGGGGGGATCTTGGCTTCCCGCTGTCTGCACGTGGACCTGCTGCACAG
CATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCCAGTGGGAACCTGGTGAACCG
CTTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCGGAGGTCATCAAGATGTTCAT
GGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATCCTGCTGGCCACGCCCATCGC
CGCCATCATCATCCCGCCCCTTGGCCTCATCTACTTCTTCGTCCAGAGGTTCTACGTGGC
TTCCTCCCGGCAGCTGAAGCGCCTCGAGTCGGTCAGCCGCTCCCCGGTCTATTCCCATTT
CAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCCTTCGAGGAGCAGGAGCGCTTCAT
CCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAGGCCTATTACCCCAGCATCGTGGC

SUBSTITUTE SHEET (RULE 26)

CAACAGGTGGCTGGCCGTGCGGCTGGAGTGTGTGGGCAACTGCATCGTTCTGTTTGCTGC
CCTGTTTGCGGTGATCTCCAGGCACAGCCTCAGTGCTGGCTTGGTGGGCCTCTCAGTGTC
TTACTCATTGCAGGTCACCACGTACTTGAACTGGCTGGTTCGGATGTCATCTGAAATGGA
AACCAACATCGTGGCCGTGGAGAGGCTCAAGGAGTATTCAGAGACTGAGAAGGAGGCGCC
CTGGCAAATCCAGGAGACAGCTCCGCCCAGCAGCTGGCCCCAGGTGGGCCGAGTGGAATT
CCGGAACTACTGCCTGCGCTACCGAGAGGACCTGGACTTCGTTCTCAGGCACATCAATGT
CACGATCAATGGGGGAGAAAAGGTCGGCATCGTGGGGCGGACGGGAGCTGGGAAGTCGTC
CCTGACCCTGGGCTTATTTCGGATCAACGAGTCTGCCGAAGGAGAGATCATCATCGATGG
CATCAACATCGCCAAGATCGGCCTGCACGACCTCCGCTTCAAGATCACCATCATCCCCCA
GGACCCTGTTTTGTTTTCGGGTTCCCTCCGAATGAACCTGGACCCATTCAGCCAGTACTC
GGATGAAGAAGTCTGGACGTCCCTGGAGCTGGCCCACCTGAAGGACTTCGTGTCAGCCCT
TCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGGGAGAACCTCAGTGTCGGGCAGCG
CCAGCTTGTGTGCCTAGCCCGGGCCCTGCTGAGGAAGACGAAGATCCTTGTGTTGGATGA
GGCCACGGCAGCCGTGGACCTGGAAACGGACGACCTCATCCAGTCCACCATCCGGACACA
GTTCGAGGACTGCACCGTCCTCACCATCGCCCACCGGCTCAACACCATCATGGACTACAC
AAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAGTACGGCGCCCCATCGGACCTCCT
GCAGCAGAGAGGTCTTTTCTACAGCATGGCCAAAGACGCCGGCTTGGTGTGAGCCCCAGA
GCTGGCATATCTGGTCAGAACTGCAGGGCCTATATGCCAGCGCCCAGGGAGGAGTCAGTA
CCCCTGGTAAACCAAGCCTCCCACACTGAAACCAAAACATAAAAACCAAACCCAGACAAC
CAAAACATATTCAAAGCAGCAGCCACCGCCATCCGGTCCCCTGCCTGGAACTGGCTGTGA
AGACCCAGGAGAGACAGAGATGCGAACCACC

ABCB6 GENBANK:AF070598

CCTTCCTGTGGATCCGGGTGCAGCAGTTCACGTCTCGGCGGGTGGAGCTGCTCATCTTCT
CCCACCTGCACGAGCTCTCACTGCGCTGGCACCTGGGGCGCCGCACAGGGGAGGTGCTGC
GGATCGCGGATCGGGGCACATCCAGTGTCACAGGGCTGCTCAGCTACCTGGTGTTCAATG
TCATCCCCACGCTGGCCGACATCATCATTGGCATCATCTACTTCAGCATGTTCTTCAACG
CCTGGTTTGGCCTCATTGTGTTCCTGTGCATGAGTCTTTACCTCACCCTGACCATTGTGG
TCACTGAGTGGAGAACCAAGTTTCGTCGTGCTATGAACACACAGGAGAACGCTACCCGGG
CACGAGCAGTGGACTCTCTGCTAAACTTCGAGACGGTGAAGTATTACAACGCCGAGAGTT
ACGAAGTGGAACGCTATCGAGAGGCCATCATCAAATATCAGGGTTTGGAGTGGAAGTCGA
GCGCTTCACTGGTTTTACTAAATCAGACCCAGAACCTGGTGATTGGGCTCGGGCTCCTCG
CCGGCTCCCTGCTTTGCGCATACTTTGTCACTGAGCAGAAGCTACAGGTTGGGGACTATG
TGCTCTTTGGCACCTACATTATCCAGCTGTACATGCCCCTCAATTGGTTTGGCACCTACT
ACAGGATGATCCAGACCAACTTCATTGACATGGAGAACATGTTTGACTTGCTGAAAGAGG
AGACAGAAGTGAAGGACCTTCCTGGAGCAGGGCCCCTTCGCTTTCAGAAGGGCCGTATTG
AGTTTGAGAACGTGCACTTCAGCTATGCCGATGGGCGGGAGACTCTGCAGGACGTGTCTT
TCACTGTGATGCCTGGACAGACACTTGCCCTGGTGGGCCCATCTGGGGCAGGGAAGAGCA

ERSATZBLATT (REGEL 26)

CAATTTTGCGCCTGCTGTTTCGCTTCTACGACATCAGCTCTGGCTGCATCCGAATAGATG
GGCAGGACATTTCACAGGTGACCCAGGCCTCTCTCCGGTCTCACATTGGAGTTGTGCCCC
AAGACACTGTCCTCTTTAATGACACCATCGCCGACAATATCCGTTACGGCCGTGTCACAG
CTGGGAATGATGAGGTGGAGGCTGCTGCTCAGGCTGCAGGCATCCATGATGCCATTATGG
CTTTCCCTGAAGGGTACAGGACACAGGTGGGCGAGCGGGGACTGAAGCTGAGCGGCGGGG
AGAAGCAGCGCGTCGCCATTGCCCGCACCATCCTCAAGGCTCCGGGCATCATTCTGCTGG
ATGAGGCAACGTCAGCGCTGGATACATCTAATGAGAGGGCCATCCAGGCTTCTCTGGCCA
AAGTCTGTGCCAACCGCACCACCATCGTAGTGGCACACAGGCTCTCAACTGTGGTCAATG
CTGACCAGATCCTCGTCATCAAGGATGGCTGCATCGTGGAGAGGGGACGACACGAGGCTC
TGTTGTCCCGAGGTGGGGTGTATGCTGACATGTGGCAGCTGCAGCAGGGACAGGAAGAAA
CCTCTGAAGACACTAAGCCTCAGACCATGGAACGGTGACAAAAGTTTGGCCACTTCCCTC
TCAAAGACTAACCCAGAAGGGAATAAGATGTGTCTCCTTTCCCTGGCTTATTTCATCCTG
GTCTTGGGGTATGGTGCTAGCTATGGTAAGGGAAAGGGACCTTTCCGAAAAACATCTTTT
GGGGAAATAAAAATGTGGACTGTGAAAAAAAAAAAAAAAAAAAA
ABCB11 GENBANK:AF091582
GAATGATGAAAACCGAGGTTGGAAAAGGTTGTGAAACCTTTTAACTCTCCACAGTGGAGT
CCATTATTTCCTCTGGCTTCCTCAAATTCATATTCACAGGGTCGTTGGCTGTGGGTTGCA
ATTACCATGTCTGACTCAGTAATTCTTCGAAGTATAAAGAAATTTGGAGAGGAGAATGAT
GGTTTTGAGTCAGATAAATCATATAATAATGATAAGAAATCAAGGTTACAAGATGAGAAG
AAAGGTGATGGCGTTAGAGTTGGCTTCTTTCAATTGTTTCGGTTTTCTTCATCAACTGAC
ATTTGGCTGATGTTTGTGGGAAGTTTGTGTGCATTTCTCCATGGAATAGCCCAGCCAGGC
GTGCTACTCATTTTTGGCACAATGACAGATGTTTTTATTGACTACGACGTTGAGTTACAA
GAACTCCAGATTCCAGGAAAAGCATGTGTGAATAACACCATTGTATGGACTAACAGTTCC
CTCAACCAGAACATGACAAATGGAACACGTTGTGGGTTGCTGAACATCGAGAGCGAAATG
ATCAAATTTGCCAGTTACTATGCTGGAATTGCTGTCGCAGTACTTATCACAGGATATATT
CAAATATGCTTTTGGGTCATTGCCGCAGCTCGTCAGATACAGAAAATGAGAAAATTTTAC
TTTAGGAGAATAATGAGAATGGAAATAGGGTGGTTTGACTGCAATTCAGTGGGGGAGCTG
AATACAAGATTCTCTGATGATATTAATAAAATCAATGATGCCATAGCTGACCAAATGGCC
CTTTTCATTCAGCGCATGACCTCGACCATCTGTGGTTTCCTGTTGGGATTTTTCAGGGGT
TGGAAACTGACCTTGGTTATTATTTCTGTCAGCCCTCTCATTGGGATTGGAGCAGCCACC
ATTGGTCTGAGTGTGTCCAAGTTTACGGACTATGAGCTGAAGGCCTATGCCAAAGCAGGG
GTGGTGGCTGATGAAGTCATTTCATCAATGAGAACAGTGGCTGCTTTTGGTGGTGAGAAA
AGAGAGGTTGAAAGGTATGAGAAAAATCTTGTGTTCGCCCAGCGTTGGGGAATTAGAAAA
GGAATAGTGATGGGATTCTTTACTGGATTCGTGTGGTGTCTCATCTTTTTGTGTTATGCA
GTGGCCTTCTGGTACGGCTCCACACTTGTCCTGGATGAAGGAGAATATACACCAGGAACC
CTTGTCCAGATTTTCCTCAGTGTCATAGTAGGAGCTTTAAATCTTGGCAATGCCTCTCCT
TGTTTGGAAGCCTTTGCAACTGGACGTGCAGCAGCCACCAGCATTTTTGAGACAATAGAC
AGGAAACCCATCATTGACTGCATGTCAGAAGATGGTTACAAGTTGGATCGAATCAAGGGT
GAAATTGAATTCCATAATGTGACCTTCCATTATCCTTCCAGACCAGAGGTGAAGATTCTA

AATGACCTCAACATGGTCATTAAACCAGGGGAAATGACAGCTCTGGTAGGACCCAGTGGA
GCTGGAAAAAGTACAGCACTGCAACTCATTCAGCGATTCTATGACCCCTGTGAAGGAATG
GTGACCGTGGATGGCCATGACATTCGCTCTCTTAACATTCAGTGGCTTAGAGATCAGATT
GGGATAGTGGAGCAAGAGCCAGTTCTGTTCTCTACCACCATTGCAGAAAATATTCGCTAT
GGCAGAGAAGATGCAACAATGGAAGACATAGTCCAAGCTGCCAAGGAGGCCAATGCCTAC
AACTTCATCATGGACCTGCCACAGCAATTTGACACCCTTGTTGGAGAAGGAGGAGGCCAG
ATGAGTGGTGGCCAGAAACAAAGGGTAGCTATCGCCAGAGCCCTCATCCGAAATCCCAAG
ATTCTGCTTTTGGACATGGCCACCTCAGCTCTGGACAATGAGAGTGAAGCCATGGTGCAA
GAAGTGCTGAGTAAGATTCAGCATGGGCACACAATCATTTCAGTTGCTCATCGCTTGTCT
ACGGTCAGAGCTGCAGATACCATCATTGGTTTTGAACATGGCACTGCAGTGGAAAGAGGG
ACCCATGAAGAATTACTGGAAAGGAAAGGTGTTTACTTCACTCTAGTGACTTTGCAAAGC
CAGGGAAATCAAGCTCTTAATGAAGAGGACATAAAGGATGCAACTGAAGATGACATGCTT
GCGAGGACCTTTAGCAGAGGGAGCTACCAGGATAGTTTAAGGGCTTCCATCCGGCAACGC
TCCAAGTCTCAGCTTTCTTACCTGGTGCACGAACCTCCATTAGCTGTTGTAGATCATAAG
TCTACCTATGAAGAAGATAGAAAGGACAAGGACATTCCTGTGCAGGAAGAAGTTGAACCT
GCCCCAGTTAGGAGGATTCTGAAATTCAGTGCTCCAGAATGGCCCTACATGCTGGTAGGG
TCTGTGGGTGCAGCTGTGAACGGGACAGTCACACCCTTGTATGCCTTTTTATTCAGCCAG
ATTCTTGGGACTTTTTCAATTCCTGATAAAGAGGAACAAAGGTCACAGATCAATGGTGTG
TGCCTACTTTTTGTAGCAATGGGCTGTGTATCTCTTTTCACCCAATTTCTACAGGGATAT
GCCTTTGCTAAATCTGGGGAGCTCCTAACAAAAAGGCTACGTAAATTTGGTTTCAGGGCA
ATGCTGGGGCAAGATATTGCCTGGTTTGATGACCTCAGAAATAGCCCTGGAGCATTGACA
ACAAGACTTGCTACAGATGCTTCCCAAGTTCAAGGGGCTGCCGGCTCTCAGATCGGGATG
ATAGTCAATTCCTTCACTAACGTCACTGTGGCCATGATCATTGCCTTCTCCTTTAGCTGG
AAGCTGAGCCTGGTCATCTTGTGCTTCTTCCCCTTCTTGGCTTTATCAGGAGCCACACAG
ACCAGGATGTTGACAGGATTTGCCTCTCGAGATAAGCAGGCCCTGGAGATGGTGGGACAG
ATTACAAATGAAGCCCTCAGTAACATCCGCACTGTTGCTGGAATTGGAAAGGAGAGGCGG
TTCATTGAAGCACTTGAGACTGAGCTGGAGAAGCCCTTCAAGACAGCCATTCAGAAAGCC
AATATTTACGGATTCTGCTTTGCCTTTGCCCAGTGCATCATGTTTATTGCGAATTCTGCT
TCCTACAGATATGGAGGTTACTTAATCTCCAATGAGGGGCTCCATTTCAGCTATGTGTTC
AGGGTGATCTCTGCAGTTGTACTGAGTGCAACAGCTCTTGGAAGAGCCTTCTCTTACACC
CCAAGTTATGCAAAAGCTAAAATATCAGCTGCACGCTTTTTTCAACTGCTGGACCGACAA
CCCCCAATCAGTGTATACAATACTGCAGGTGAAAAATGGGACAACTTCCAGGGGAAGATT
GATTTTGTTGATTGTAAATTTACATATCCTTCTCGACCTGACTCGCAAGTTCTGAATGGT
CTCTCAGTGTCGATTAGTCCAGGGCAGACACTGGCGTTTGTTGGGAGCAGTGGATGTGGC
AAAAGCACTAGCATTCAGCTGTTGGAACGTTTCTATGATCCTGATCAAGGGAAGGTGATG
ATAGATGGTCATGACAGCAAAAAAGTAAATGTCCAGTTCCTCCGCTCAAACATTGGAATT
GTTTCCCAGGAACCAGTGTTGTTTGCCTGTAGCATAATGGACAATATCAAGTATGGAGAC
AACACCAAAGAAATTCCCATGGAAAGAGTCATAGCAGCTGCAAAACAGGCTCAGCTGCAT
GATTTTGTCATGTCACTCCCAGAGAAATATGAAACTAACGTTGGGTCCCAGGGGTCTCAA

SUBSTITUTE SHEET (RULE 26)

CTCTCTAGAGGGGAGAAACAACGCATTGCTATTGCTCGGGCCATTGTACGAGATCCTAAA
ATCTTGCTACTAGATGAAGCCACTTCTGCCTTAGACACAGAAAGTGAAAAGACGGTGCAG
GTTGCTCTAGACAAAGCCAGAGAGGGTCGGACCTGCATTGTCATTGCCCATCGCTTGTCC
ACCATCCAGAACGCGGATATCATTGCTGTCATGGCACAGGGGGTGGTGATTGAAAAGGGG
ACCCATGAAGAACTGATGGCCCAAAAAGGAGCCTACTACAAACTAGTCACCACTGGATCC
CCCATCAGTTGACCCAATGCAAGAATCTCAGACACACATGACGCACCAGTTACAGGGGTT
GTTTTTAAAGAAAAAAACAATCCCAGCACGAGGGATTGCTGGGATTGTTTTTTCTTTAAA
GAAGAATNTNNNTATTTTACTTTTACNNNCNTTTTCCTACATCGGAATCCAANCTAATTT
CTAATGGCCTTCCATAATAATTCTGCTTTAGATGTGTATACAGAAAATGAAAGAAACTAG
GGTCCATGTGAGGGAAAACCCAATGTCAAGTGGCAGCTCAGCCACCACTCAGTGCTTCTC
TGTGCAGGAGCCAGTCCTGATTAATATGTGGGAATTAGTGAGACATCAGGGAGTAAGTGA
CACTTTGAACTCCTCAAGGACAGAGAACTGTCTTTCATTTTTGAACCCTCGGTGTACACA
GAGGCGGGTCTGTAACAGGCAATCAACAAACGTTTCTTGAGCTAGACCAAGGTCAGATTT
GAAAAGAACAGAAGGACTGAAGACCAGCTGTGTTTCTTAACTAAATTTGTCTTTCAAGTG
AAACCAGCTTCCTTCATCTCTAAGGCTAAGGATAGGGAAAGGGTGGGATGCTCTCANGCT
GAGGGAGGCANAAAGGGAAAGTATTANCATGAGCTTTCCANTTAGGGCTGTTGATTTATG
CTTTAACTTCANANTGAGTGTAGGGTGGTGANNCTA

ABCG2 GENBANK:AF103796

TTTAGGAACGCACCGTGCACATGCTTGGTGGTCTTGTTAAGTGGAAACTGCTGCTTTAGA
GTTTGTTTGGAAGGTCCGGGTGACTCATCCCAACATTTACATCCTTAATTGTTAAAGCGC
TGCCTCCGAGCGCACGCATCCTGAGATCCTGAGCCTTTGGTTAAGACCGAGCTCTATTAA
GCTGAAAAGATAAAAACTCTCCAGATGTCTTCCAGTAATGTCGAAGTTTTTATCCCAGTG
TCACAAGGAAACACCAATGGCTTCCCCGCGACAGTTTCCAATGACCTGAAGGCATTTACT
GAAGGAGCTGTGTTAAGTTTTCATAACATCTGCTATCGAGTAAAACTGAAGAGTGGCTTT
CTACCTTGTCGAAAACCAGTTGAGAAAGAAATATTATCGAATATCAATGGGATCATGAAA
CCTGGTCTCAACGCCATCCTGGGACCCACAGGTGGAGGCAAATCTTCGTTATTAGATGTC
TTAGCTGCAAGGAAAGATCCAAGTGGATTATCTGGAGATGTTCTGATAAATGGAGCACCG
CGACCTGCCAATTTCAAATGTAATTCAGGTTACGTGGTACAAGATGATGTTGTGATGGGC
ACTCTGACGGTGAGAGAAAACTTACAGTTCTCAGCAGCTCTTCGGCTTGCAACAACTATG
ACGAATCATGAAAAAAACGAACGGATTAACAGGGTCATTGAAGAGTTAGGTCTGGATAAA
GTGGCAGACTCCAAGGTTGGAACTCAGTTTATCCGTGGTGTGTCTGGAGGAGAAAGAAAA
AGGACTAGTATAGGAATGGAGCTTATCACTGATCCTTCCATCTTGTCCTTGGATGAGCCT
ACAACTGGCTTAGACTCAAGCACAGCAAATGCTGTCCTTTTGCTCCTGAAAAGGATGTCT
AAGCAGGGACGAACAATCATCTTCTCCATTCATCAGCCTCGATATTCCATCTTCAAGTTG
TTTGATAGCCTCACCTTATTGGCCTCAGGAAGACTTATGTTCCACGGGCCTGCTCAGGAG
GCCTTGGGATACTTTGAATCAGCTGGTTATCACTGTGAGGCCTATAATAACCCTGCAGAC
TTCTTCTTGGACATCATTAATGGAGATTCCACTGCTGTGGCATTAAACAGAGAAGAAGAC
TTTAAAGCCACAGAGATCATAGAGCCTTCCAAGCAGGATAAGCCACTCATAGAAAAATTA
GCGGAGATTTATGTCAACTCCTCCTTCTACAAAGAGACAAAAGCTGAATTACATCAACTT

SUBSTITUTE SHEET (RULE 26)

TCCGGGGGTGAGAAGAAGAAGAAGATCACAGTCTTCAAGGAGATCAGCTACACCACCTCC
TTCTGTCATCAACTCAGATGGGTTTCCAAGCGTTCATTCAAAAACTTGCTGGGTAATCCC
CAGGCCTCTATAGCTCAGATCATTGTCACAGTCGTACTGGGACTGGTTATAGGTGCCATT
TACTTTGGGCTAAAAAATGATTCTACTGGAATCCAGAACAGAGCTGGGGTTCTCTTCTTC
CTGACGACCAACCAGTGTTTCAGCAGTGTTTCAGCCGTGGAACTCTTTGTGGTAGAGAAG
AAGCTCTTCATACATGAATACATCAGCGGATACTACAGAGTGTCATCTTATTTCCTTGGA
AAACTGTTATCTGATTTATTACCCATGAGGATGTTACCAAGTATTATATTTACCTGTATA
GTGTACTTCATGTTAGGATTGAAGCCAAAGGCAGATGCCTTCTTCGTTATGATGTTTACC
CTTATGATGGTGGCTTATTCAGCCAGTTCCATGGCACTGGCCATAGCAGCAGGTCAGAGT
GTGGTTTCTGTAGCAACACTTCTCATGACCATCTGTTTTGTGTTTATGATGATTTTTTCA
GGTCTGTTGGTCAATCTCACAACCATTGCATCTTGGCTGTCATGGCTTCAGTACTTCAGC
ATTCCACGATATGGATTTACGGCTTTGCAGCATAATGAATTTTTGGGACAAAACTTCTGC
CCAGGACTCAATGCAACAGGAAACAATCCTTGTAACTATGCAACATGTACTGGCGAAGAA
TATTTGGTAAAGCAGGGCATCGATCTCTCACCCTGGGGCTTGTGGAAGAATCACGTGGCC
TTGGCTTGTATGATTGTTATTTTCCTCACAATTGCCTACCTGAAATTGTTATTTCTTAAA
AAATATTCTTAAATTTCCCCTTAATTCAGTATGATTTATCCTCACATAAAAAAGAAGCAC
TTTGATTGAAGTATTCAATCAAGTTTTTTTGTTGTTTTCTGTTCCCTTGCCATCACACTG
TTGCACAGCAGCAATTGTTTTAAAGAGATACATTTTTAGAAATCACAACAAACTGAATTA
AACATGAAAGAACCCAAGACATCATGTATCGCATATTAGTTAATCTCCTCAGACAGTAAC
CATGGGGAAGAAATCTGGTCTAATTTATTAATCTAAAAAAGGAGAATTGAATTCTGGAAA
CTCCTGACAAGTTATTACTGTCTCTGGCATTTGTTTCCTCATCTTTAAAATGAATAGGTA
GGTTAGTAGCCCTTCAGTCTTAATACTTTATGATGCTATGGTTTGCCATTATTTAATATA
TGACAAATGTATTAATGCTATACTGGAAATGTAAAATTGAAAATATGTTGGAAAAAAGAT
TCTGTCTTATAGGGTAAAAAAAGCCACCGGTGATAGAAAAAAAATCTTTTTGATAAGCAC
ATTAAAGTTAATAGAACTT

ABCC5 GENBANK:AF104942

CCGGGCAGGTGGCTCATGCTCGGGAGCGTGGTTGAGCGGCTGGCGCGGTTGTCCTGGAGC
AGGGGCGCAGGAATTCTGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCGCTCAG
AGAAGATGAAGGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAA
GTGTGAGGGAGAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCA
GGAGAACTCGACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCC
TCTCTCTTGATGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGG
GAAAGTACCATCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTCCAAACACCAGC
ACCCAGTGGACAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGG
CCCGTGTGGCCCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGC
ACGAGTCTTCTGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATG
AAGTTGGGCCAGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGC
TCATCCTGTCCATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCT
TCATGGTGAAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCT

SUBSTITUTE SHEET (RULE 26)

TGTTGTTAGTGCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGA
CTTGGGCATTGAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCAT
TTAAGAAGATCCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACA
TTTGCTCCAACGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTG
GAGGACCCGTTGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAG
GCTTCCTGGGATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGC
TCACAGCATATTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGA
ATGAAGTTCTTACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTC
AGAGTGTTCAAAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCC
AGGGTATCACTGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCT
CTGTTCATATGACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAG
TCTTCAATTCCATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAG
AAGCCTCAGTGGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGA
TAAAGAACAAACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCAT
GGGACTCCTCCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAG
ACAAGAGGGCTTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATC
AGGCGGTGCTGGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTC
CCGAAGAGGAAGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGC
ACAGCATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAA
GTGGAAAAACCTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCA
TTGCAATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTC
TGAGAGACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGA
ACAGCTGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTG
GAGAGCGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCT
TGTATAGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATG
TGGGCAACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGT
TTGTTACCCACCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGG
GCTGTATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTA
CCATTTTTAATAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGG
AAACCAGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAGTAAAGA
AGGAAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGG
GTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCAT
TCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGT
GGTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGA
CCTCGGTGAGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACG
CCCTCTCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGG
GCACGCTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCC
CTATGAAGTTTTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACA
TGGATGAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCC

SUBSTITUTE SHEET (RULE 26)

TGGTGTTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGG
GGCCCCTTGTCATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGC
TGAAGCGTCTGGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATAC
AGGGCCTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGG
AGCTGCTGGATGACAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGG
CTGTGCGGCTGGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTC
TTATGCACGGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGT
TAACGGGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCT
CGGTGGAGAGGATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTA
AGAACAAGGCTCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAG
AGATGAGGTACCGAGAAAACCTCCCTCTTGTCCTAAAGAAAGTATCCTTCACGATCAAAC
CTAAAGAGAAGATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGG
CCCTCTTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCA
GTGATATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGC
TGTTCAGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGA
TTTGGGATGCCCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAAC
TTGAATCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGT
GCATAGCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTG
CCATGGACACAGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACT
GTACCATGCTGACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGG
TGCTGGCCCAGGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACA
GTTCCCGATTCTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGAC
TCCTCCCTGTTGACGAAGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGG
CCCCTCATCGCGTCCTCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCA
GTTCCGGATTGGCTTGTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTT
ATTCCATATTCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCA
GGGAACCGTTATTATAATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATA
TCTATATATAATTCTGTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTA
TATTAAAATAAGCACTGTGCTAATAACAGTGCATATTCCTTTCTATCATTTTTGTACAGT
TTGCTGTACTAGAGATCTGGTTTTGCTATTAGACTGTAGGAAGAGTAGCATTTCATTCTT
CTCTAGCTGGTGGTTTCACGGTGCCAGGTTTTCTGGGTGTCCAAAGGAAGACGTGTGGCA
ATAGTGGGCCCTCCGACAGCCCCCTCTGCCGCCTCCCCACAGCCGCTCCAGGGGTGGCTG
GAGACGGGTGGGCGGCTGGAGACCATGCAGAGCGCCGTGAGTTCTCAGGGCTCCTGCCTT
CTGTCCTGGTGTCACTTACTGTTTCTGTCAGGAGAGCAGCGGGGCGAAGCCCAGGCCCCT
TTTCACTCCCTCCATCAAGAATGGGGATCACAGAGACATTCCTCCGAGCCGGGGAGTTTC
TTTCCTGCCTTCTTCTTTTTGCTGTTGTTTCTAAACAAGAATCAGTCTATCCACAGAGAG
TCCCACTGCCTCAGGTTCCTATGGCTGGCCACTGCACAGAGCTCTCCAGCTCCAAGACCT
GTTGGTTCCAAGCCCTGGAGCCAACTGCTGCTTTTTGAGGTGGCACTTTTTCATTTGCCT
ATTCCCACACCTCCACAGTTCAGTGGCAGGGCTCAGGATTTCGTGGGTCTGTTTTCCTTT

SUBSTITUTE SHEET (RULE 26)

CTCACCGCAGTCGTCGCACAGTCTCTCTCTCTCTCCCCTCAAAGTCTGCAACTTTAAG
CAGCTCTTGCTAATCAGTGTCTCACACTGGCGTAGAAGTTTTTGTACTGTAAAGAGACCT
ACCTCAGGTTGCTGGTTGCTGTGTGGTTTGGTGTGTTCCCGCAAACCCCCTTTGTGCTGT
GGGGCTGGTAGCTCAGGTGGGCGTGGTCACTGCTGTCATCAGTTGAATGGTCAGCGTTGC
ATGTCGTGACCAACTAGACATTCTGTCGCCTTAGCATGTTTGCTGAACACCTTGTGGAAG
CAAAAATCTGAAAATGTGAATAAAATTATTTTGGATTTTGTAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAA

ABCA5 Acc.Nr.: AF000148 GENBANK:HSAF000148

GCCAGAGGCGCTCTTAACGGCGTTTATGTCCTTTGCTGTCTGAGGGGCCTCAGCTCTGAC
CAATCTGGTCTTCGTGTGGTCATTAGCATGGGCTTCGTGAGACAGATACAGCTTTTGCTC
TGGAAGAACTGGACCCTGCGGAAAAGGCAAAAGATTCGCTTTGTGGTGGAACTCGTGTGG
CCTTTATCTTTATTTCTGGTCTTGATCTGGTTAAGGAATGCCAACCCGCTCTACAGCCAT
CATGAATGCCATTTCCCCAACAAGGCGATGCCCTCAGCAGGAATGCTGCCGTGGCTCCAG
GGGATCTTCTGCAATGTGAACAATCCCTGTTTTCAAAGCCCCACCCCAGGAGAATCTCCT
GGAATTGTGTCAAACTATAACAACTCCATCTTGGCAAGGGTATATCGAGATTTTCAAGAA
CTCCTCATGAATGCACCAGAGAGCCAGCACCTTGGCCGTATTTGGACAGAGCTACACATC
TTGTCCCAATTCATGGACACCCTCCGGACTCACCCGGAGAGAATTGCAGGAAGAGGAATA
CGAATAAGGGATATCTTGAAAGATGAAGAAACACTGACACTATTTCTCATTAAAAACATC
GGCCTGTCTGACTCAGTGGTCTACCTTCTGATCAACTCTCAAGTCCGTCCAGAGCAGTTC
GCTCATGGAGTCCCGGACCTGGCGCTGAAGGACATCGCCTGCAGCGAGGCCCTCCTGGAG
CGCTTCATCATCTTCAGCCAGAGACGCGGGGCAAAGACGGTGCGCTATGCCCTGTGCTCC
CTCTCCCAGGGCACCCTACAGTGGATAGAAGACACTCTGTATGCCAACGTGGACTTCTTC
AAGCTCTTCCGTGTGCTTCCCACACTCCTAGACAGCCGTTCTCAAGGTATCAATCTGAGA
TCTTGGGGAGGAATATTATCTGATATGTCACCAAGAATTCAAGAGTTTATCCATCGGCCG
AGTATGCAGGACTTGCTGTGGGTGACCAGGCCCCTCATGCAGAATGGTGGTCCAGAGACC
TTTACAAAGCTGATGGGCATCCTGTCTGACCTCCTGTGTGGCTACCCCGAGGGAGGTGGC
TCTCGGGTGCTCTCCTTCAACTGGTATGAAGACAATAACTATAAGGCCTTTCTGGGGATT
GACTCCACAAGGAAGGATCCTATCTATTCTTATGACAGAAGAACAACATCCTTTTGTAAT
GCATTGATCCAGAGCCTGGAGTCAAATCCTTTAACCAAAATCGCTTGGAGGGCGGCAAAG
CCTTTGCTGATGGGAAAAATCCTGTACACTCCTGATTCACCTGCAGCACGAAGGATACTG
AAGAATGCCAACTCAACTTTTGAAGAACTGGAACACGTTAGGAAGTTGGTCAAAGCCTGG
GAAGAAGTAGGGCCCCAGATCTGGTACTTCTTTGACAACAGCACACAGATGAACATGATC
AGAGATACCCTGGGGAACCCAACAGTAAAAGACTTTTTGAATAGGCAGCTTGGTGAAGAA
GGTATTACTGCTGAAGCCATCCTAAACTTCCTCTACAAGGGCCCTCGGGAAAGCCAGGCT
GACGACATGGCCAACTTCGACTGGAGGGACATATTTAACATCACTGATCGCACCCTCCGC
CTGGTCAATCAATACCTGGAGTGCTTGGTCCTGGATAAGTTTGAAAGCTACAATGATGAA
ACTCAGCTCACCCAACGTGCCCTCTCTCTACTGGAGGAAAACATGTTCTGGGCCGGAGTG
GTATTCCCTGACATGTATCCCTGGACCAGCTCTCTACCACCCCACGTGAAGTATAAGATC
CGAATGGACATAGACGTGGTGGAGAAAACCAATAAGATTAAAGACAGGTATTGGGATTCT

SUBSTITUTE SHEET (RULE 26)

GGTCCCAGAGCTGATCCCGTGGAAGATTTCCGGTACATCTGGGGCGGGTTTGCCTATCTG
CAGGACATGGTTGAACAGGGGATCACAAGGAGCCAGGTGCAGGCGGAGGCTCCAGTTGGA
ATCTACCTCCAGCAGATGCCCTACCCCTGCTTCGTGGACGATTCTTTCATGATCATCCTG
AACCGCTGTTTCCCTATCTTCATGGTGCTGGCATGGATCTACTCTGTCTCCATGACTGTG
AAGAGCATCGTCTTGGAGAAGGAGTTGCGACTGAAGGAGACCTTGAAAAATCAGGGTGTC
TCCAATGCAGTGATTTGGTGTACCTGGTTCCTGGACAGCTTCTCCATCATGTCGATGAGC
ATCTTCCTCCTGACGATATTCATCATGCATGTAAGAATCCTACATTACAGCGACCCATTC
ATCCTCTTCCTGTTCTTGTTGGCTTTCTCCACTGCCACCATCATGCTGTGCTTTCTGCTC
AGCACCTTCTTCTCCAAGGCCAGTCTGGCAGCAGCCTGTAGTGGTGTCATCTATTTCACC
CTCTACCTGCCACACATCCTGTGCTTCGCCTGGCAGGACCGCATGACCGCTGAGCTGAAG
AAGGCTGTGAGCTTACTGTCTCCGGTGGCATTTGGATTTGGCACTGAGTACCTGGTTCGC
TTTGAAGAGCAAGGCCTGGGGCTGCAGTGGAGCAACATCGGGAACAGTCCCACGGAAGGG
GACGAATTCAGCTTCCTGCTGTCCATGCAGATGATGCTCCTTGATGCTGCTGTCTATGGC
TTACTCGCTTGGTACCTTGATCAGGTGTTTCCAGGAGACTATGGAACCCCACTTCCTTGG
TACTTTCTTCTACAAGAGTCGTATTGGCTTGGCGGTGAAGGGTGTTCAACCAGAGAAGAA
AGAGCCCTGGAAAAGACCGAGCCCCTAACAGAGGAAACGGAGGATCCAGAGCACCCAGAA
GGAATACACGACTCCTTCTTTGAACGTGAGCATCCAGGGTGGGTTCCTGGGGTATGCGTG
AAGAATCTGGTAAAGATTTTTGAGCCCTCCGGCCGGCCAGCTGTGGACCGTCTGAACATC
ACCTTCTACGAGAACCAGATCACCGCATTCCTGGGCCACAATGGAGCTGGGAAAACCACC
ACCTTGTCCATCCTGACGGGTCTGTTGCCACCAACCTCTGGGACTGTGCTCGTTGGGGGA
AGGGACATTGAAACCAGCCTGGATGCAGTCCGGCAGAGCCTTGGCATGTGTCCACAGCAC
AACATCCTGTTCCACCACCTCACGGTGGCTGAGCACATGCTGTTCTATGCCCAGCTGAAA
GGAAAGTCCCAGGAGGAGGCCCAGCTGGAGATGGAAGCCATGTTGGAGGACACAGGCCTC
CACCACAAGCGGAATGAAGAGGCTCAGGACCTATCAGGTGGCATGCAGAGAAAGCTGTCG
GTTGCCATTGCCTTTGTGGGAGATGCCAAGGTGGTGATTCTGGACGAACCCACCTCTGGG
GTGGACCCTTACTCGAGACGCTCAATCTGGGATCTGCTCCTGAAGTATCGCTCAGGCAGA
ACCATCATCATGTCCACTCACCACATGGACGAGGCCGACCTCCTTGGGGACCGCATTGCC
ATCATTGCCCAGGGAAGGCTCTACTGCTCAGGCACCCCACTCTTCCTGAAGAACTGCTTT
GGCACAGGCTTGTACTTAACCTTGGTGCGCAAGATGAAAAACATCCAGAGCCAAAGGAAA
GGCAGTGAGGGGACCTGCAGCTGCTCGTCTAAGGGTTTCTCCACCACGTGTCCAGCCCAC
GTCGATGACCTAACTCCAGAACAAGTCCTGGATGGGGATGTAAATGAGCTGATGGATGTA
GTTCTCCACCATGTTCCAGAGGCAAAGCTGGTGGAGTGCATTGGTCAAGAACTTATCTTC
CTTCTTCCAAATAAGAACTTCAAGCACAGAGCATATGCCAGCCTTTTCAGAGAGCTGGAG
GAGACGCTGGCTGACCTTGGTCTCAGCAGTTTTGGAATTTCTGACACTCCCCTGGAAGAG
ATTTTTCTGAAGGTCACGGAGGATTCTGATTCAGGACCTCTGTTTGCGGGTGGCGCTCAG
CAGAAAAGAGAAAACGTCAACCCCCGACACCCCTGCTTGGGTCCCAGAGAGAAGGCTGGA
CAGACACCCCAGGACTCCAATGTCTGCTCCCCAGGGGCGCCGGCTGCTCACCCAGAGGGC
CAGCCTCCCCCAGAGCCAGAGTGCCCAGGCCCGCAGCTCAACACGGGGACACAGCTGGTC
CTCCAGCATGTGCAGGCGCTGCTGGTCAAGAGATTCCAACACACCATCCGCAGCCACAAG

SUBSTITUTE SHEET (RULE 26)

GACTTCCTGGCGCAGATCGTGCTCCCGGCTACCTTTGTGTTTTTGGCTCTGATGCTTTCT

ATTGTTATCCCTCCTTTTGGCGAATACCCCGCTTTGACCCTTCACCCCTGGATATATGGG

CAGCAGTACACCTTCTTCAGCATGGATGAACCAGGCAGTGAGCAGTTCACGGTACTTGCA

GACGTCCTCCTGAATAAGCCAGGCTTTGGCAACCGCTGCCTGAAGGAAGGGTGGCTTCCG

GAGTACCCCTGTGGCAACTCAACACCCTGGAAGACTCCTTCTGTGTCCCCAAACATCACC

CAGCTGTTCCAGAAGCAGAAATGGACACAGGTCAACCCTTCACCATCCTGCAGGTGCAGC

ACCAGGGAGAAGCTCACCATGCTGCCAGAGTGCCCCGAGGGTGCCGGGGGCCTCCCGCCC

CCCCAGAGAACACAGCGCAGCACGGAAATTCTACAAGACCTGACGGACAGGAACATCTCC

GACTTCTTGGTAAAAACGTATCCTGCTCTTATAAGAAGCAGCTTAAAGAGCAAATTCTGG

GTCAATGAACAGAGGTATGGAGGAATTTCCATTGGAGGAAAGCTCCCAGTCGTCCCCATC

ACGGGGGAAGCACTTGTTGGGTTTTTAAGCGACCTTGGCCGGATCATGAATGTGAGCGGG

GGCCCTATCACTAGAGAGGCCTCTAAAGAAATACCTGATTTCCTTAAACATCTAGAAACT

GAAGACAACATTAAGGTGTGGTTTAATAACAAAGGCTGGCATGCCCTGGTCAGCTTTCTC

AATGTGGCCCACAACGCCATCTTACGGGCCAGCCTGCCTAAGGACAGGAGCCCCGAGGAG

TATGGAATCACCGTCATTAGCCAACCCCTGAACCTGACCAAGGAGCAGCTCTCAGAGATT

ACAGTGCTGACCACTTCAGTGGATGCTGTGGTTGCCATCTGTGTGATTTTCTCCATGTCC

TTCGTCCCAGCCAGCTTTGTCCTTTATTTGATCCAGGAGCGGGTGAACAAATCCAAGCAC

CTCCAGTTTATCAGTGGAGTGAGCCCCACCACCTACTGGGTGACCAACTTCCTCTGGGAC

ATCGTGAATTATTCCGTGAGTGCTGGGCTGGTGGTGGGCATCTTCATCGGGTTTCAGAAG

AAAGCCTACACTTCTCCAGAAAACCTTCCTGCCCTTGTGGCACTGCTCCTGCTGTATGGA

TGGGCGGTCATTCCCATGATGTACCCAGCATCCTTCCTGTTTGATGTCCCCAGCACAGCC

TATGTGGCTTTATCTTGTGCTAATCTGTTCATCGGCATCAACAGCAGTGCTATTACCTTC

ATCTTGGAATTATTTGAGAATAACCGGACGCTGCTCAGGTTCAACGCCGTGCTGAGGAAG

CTGCTCATTGTCTTCCCCCACTTCTGCCTGGGCCGGGGCCTCATTGACCTTGCACTGAGC

CAGGCTGTGACAGATGTCTATGCCCGGTTTGGTGAGGAGCACTCTGCAAATCCGTTCCAC

TGGGACCTGATTGGGAAGAACCTGTTTGCCATGGTGGTGGAAGGGGTGGTGTACTTCCTC

CTGACCCTGCTGGTCCAGCGCCACTTCTTCCTCTCCCAATGGATTGCCGAGCCCACTAAG

GAGCCCATTGTTGATGAAGATGATGATGTGGCTGAAGAAAGACAAAGAATTATTACTGGT

GGAAATAAAACTGACATCTTAAGGCTACATGAACTAACCAAGATTTATCCGGGCACCTCC

AGCCCAGCAGTGGACAGGCTGTGTGTCGGAGTTCGCCCTGGAGAGTGCTTTGGCCTCCTG

GGAGTGAATGGTGCCGGCAAAACAACCACATTCAAGATGCTCACTGGGGACAACACAGTG

ACCTCAGGGGATGCCACCGTAGCAGGCAAGAGTATTTTAACCAATATTTCTGAAGTCCAT

CAAAATATGGGCTACTGTCCTCAGTTTGATGCAATCGATGAGCTGCTCACAGGACGAGAA

CATCTTTACCTTTATGCCCGGCTTCGAGGTGTACCAGCAGAAGAAATCGAAAAGGTTGCA

AACTGGAGTATTAAGAGCCTGGGCCTGACTGTCTACGCCGACTGCCTGGCTGGCACGTAC

AGTGGGGGCAACAAGCGGAAACTCTCCACAGCCATCGCACTCATTGGCTGCCCACCGCTG

GTGCTGCTGGATGAGCCCACCACAGGGATGGACCCCCAGGCACGCCGCATGCTGTGGAAC

GTCATCGTGAGCATCATCAGAGAAGGGAGGGCTGTGGTCCTCACATCCCACAGCATGGAA

GAATGTGAGGCACTGTGTACCCGGCTGGCCATCATGGTAAAGGGCGCCTTTCGATGTATG

SUBSTITUTE SHEET (RULE 26)

GGCACCATTCAGCATCTCAAGTCCAAATTTGGAGATGGCTATATCGTCACAATGAAGATC
AAATCCCCGAAGGACGACCTGCTTCCTGACCTGAACCCTGTGGAGCAGTTCTTCCAGGGG
AACTTCCCAGGCAGTGTGCAGAGGGAGAGGCACTACAACATGCTCCAGTTCCAGGTCTCC
TCCTCCTCCCTGGCGAGGATCTTCCAGCTCCTCCTCTCCCACAAGGACAGCCTGCTCATC
GAGGAGTACTCAGTCACACAGACCACACTGGACCAGGTGTTTGTAAATTTTGCTAAACAG
CAGACTGAAAGTCATGACCTCCCTCTGCACCCTCGAGCTGCTGGAGCCAGTCGACAAGCC
CAGGACTGATCTTTCACACCGTTCGTTCCTGCAGCCAGAAAGGAACTCTGGGCAGCTGGA
GGCGCAGGAGCCTGTGCCCATATGGTCATCCAAATGGACTGGCCAGCGTAAATGACCCCA
CTGCAGCAGAAAACAAACACACGAGGAGCATGCAGCGAATTCAGAAAGAGGTCTTTCAGA
AGGAAACCGAAACTGACTTGCTCACCTGGAACACCTGATGGTGAAACCAAACAAATACAA
AATCCTTCTCCAGACCCCAGAACTAGAAACCCCGGGCCATCCCACTAGCAGCTTTGGCCT
CCATATTGCTCTCATTTCAAGCAGATCTGCTTTTCTGCATGTTTGTCTGTGTGTCTGCGT
TGTGTGTGATTTTCATGGAAAAATAAAATGCAAATGCACTCATCACAAAAAAAAAAAAAA
AAA

ABCG1 Acc.Nr.: U34919 GENBANK:HSU34919

GAATTCCGGGATGTGGAACGGTCGCAGGAGGCTGCTACAAGCCCCATGAGCAAGGCTGTT
CCCACTGACAGAGCTTTCCCAGGATGACAGAGAGTGCGCTCTGCCTCTCTGGGGTGTGCT
AGCCTACGAGGGGCAATCGTAAGGCGAATGTCACTGAAAGAACACAAGTGTCCTTAAACA
TGGACTATCTGGGCTTTCTAGTGCTGAAATTCTTCCCACTCCCACTGCCCACTTCCCATT
ATATAAAAAACACAGTTGTTTCATGTTTTTGTTTCTTTACTGTTTTTCTTTGTTTTTGTT
AAGAATGCATTCATTTATTCAAAATTGTTTATTGTAGAATAATCAGGCATTGCGTGGATG
AGGTGGTGTCCAGCAACATGGAGGCCACTGAGACGGACCTGCTGAATGGACATCTGAAAA
AAGTAGATAATAACCTCACGGAAGCCCAGCGCTTCTCCTCCTTGCCTCGGAGGGCAGCTG
TGAACATTGAATTCAGGGACCTTTCCTATTCGGTTCCTGAAGGACCCTGGTGGAGGAAGA
AAGGATACAAGACCCTCCTGAAAGGAATTTCCGGGAAGTTCAATAGTGGTGAGTTGGTGG
CCATTATGGGTCCTTCCGGGGCCGGGAAGTCCACGCTGATGAACATCCTGGCTGGATACA
GGGAGACGGGCATGAAGGGGGCCGTCCTCATCAACGGCCTGCCCCGGGACCTGCGCTGCT
TCCGGAAGGTGTCCTGCTACATCATGCAGGATGACATGCTGCTGCCGCATCTCACTGTGC
AGGAGGCCATGATGGTGTCGGCACATCTGAAGCTTCAGGAGAAGGATGAAGGCAGAAGGG
AAATGGTCAAGGAGATACTGACAGCGCTGGGCTTGCTGTCTTGCGCCAACACGCGGACCG
GGAGCCTGTCAGGTGGTCAGCGCAAGCGCCTGGCCATCGCGCTGGAGCTGGTGAACAACC
CTCCAGTCATGTTCTTCGATGAGCCCACCAGCGGCCTGGACAGCGCCTCCTGCTTCCAGG
TGGTCTCGCTGATGAAAGGGCTCGCTCAAGGGGGTCGCTCCATCATTTGCACCATCCACC
AGCCCAGCGCCAAACTCTTCGAGCTGTTCGACCAGCTTTACGTCCTGAGTCAAGGACAAT
GTGTGTACCGGGGAAAAGTCTGCAATCTTGTGCCATATTTGAGGGATTTGGGTCTGAACT
GCCCAACCTACCACAACCCAGCAGATTTTGTCATGGAGGTTGCATCCGGCGAGTACGGTG
ATCAGAACAGTCGGCTGGTGAGAGCGGTTCGGGAGGGCATGTGTGACTCAGACCACAAGA
GAGACCTCGGGGGTGATGCCGAGGTGAACCCTTTTCTTTGGCACCGGCCCTCTGAAGAGG
TAAAGCAGACAAAACGATTAAAGGGGTTGAGAAAGGACTCCTCGTCCATGGAAGGCTGCC

SUBSTITUTE SHEET (RULE 26)

ACAGCTTCTCTGCCAGCTGCCTCACGCAGTTCTGCATCCTCTTCAAGAGGACCTTCCTCA
GCATCATGAGGGACTCGGTCCTGACACACCTGCGCATCACCTCGCACATTGGGATCGGCC
TCCTCATTGGCCTGCTGTACTTGGGGATCGGGAACGAAGCCAAGAAGGTCTTGAGCAACT
CCGGCTTCCTCTTCTTCTCCATGCTGTTCCTCATGTTCGCGGCCCTCATGCCTACTGTTC
TGACATTTCCCCTGGAGATGGGAGTCTTTCTTCGGGAACACCTGAACTACTGGTACAGCC
TGAAGGCCTACTACCTGGCCAAGACCATGGCAGACGTGCCCTTTCAGATCATGTTCCCAG
TGGCCTACTGCAGCATCGTGTACTGGATGACGTCGCAGCCGTCCGACGCCGTGGCCTTTG
TGCTGTTTGCCGCGCTGGGCACCATGACCTCCCTGGTGGCACAGTCCCTGGGCCTGCTGA
TCGGAGCCGCCTCCACGTCCCTGCAGGTGGCCACTTTCGTGGGCCCAGTGACAGCCATCC
CGGTGCTCCTGTTCTCGGGGTTCTTCGTCAGCTTCGACACCATCCCCACGTACCTACAGT
GGATGTCCTACATCTCCTATGTCAGGTATGGGTTCGAAGGGGTCATCCTCTCCATCTATG
GCTTAGACCGGGAAGATCTGCACTGTGACATCGACGAGACGTGCCACTTCCAGAAGTCGG
AGGCCATCCTGCGGGAGCTGGACGTGGAAAATGCCAAGCTGTACCTGGACTTCATCGTAC
TCGGGATTTTCTTCATCTCCCTCCGCCTCATTGCCTATTTTGTCCTCAGGTACAAAATCC
GGGCAGAGAGGTAAAACACCTGAATGCCAGGAAACAGGAAGATTAGACACTGTGGCCGAG
GGCACGTCTAGAATCGAGGAGGCAAGCCTGTGCCCGACCGACGACACAGAGACTCTTCTG
ATCCAACCCCTAGAACCGCGTTGGGTTTGTGGGTGTCTCGTGCTCAGCCACTCTGCCCAG
CTGGGTTGGATCTTCTCTCCATTCCCCTTTCTAGCTTTAACTAGGAAGATGTAGGCAGAT
TGGTGGTTTTTTTTTTTTTTTAACATACAGAATTTTAAATACCACAACTGGGGCAGAATT
TAAAGCTGCAACACAGCTGGTGATGAGAGGCTTCCTCAGTCCAGTCGCTCCTTAGCACCA
GGCACCGTGGGTCCTGGATGGGGAACTGCAAGCAGCCTCTCAGCTGATGGCTGCGCAGTC
AGATGTCTGGTGGCAGAGAGTCCGAGCATGGAGCGATTCCATTTT

ABCA3 Acc.Nr: U78735 GENBANK:HSU78735

CCGCCCCGGCGCCCAGGCTCGGTGCTGGAGAGTCATGCCTGTGAGCCCTGGGCACCTCCT
GATGTCCTGCGAGGTCACGGTGTTCCCAAACCTCAGGGTTGCCCTGCCCCACTCCAGAGG
CTCTCAGGCCCCACCCCGGAGCCCTCTGTGCGGAGCCGCCTCCTCCTGGCCAGTTCCCCA
GTAGTCCTGAAGGGAGACCTGCTGTGTGGAGCCTCTTCTGGGACCCAGCCATGAGTGTGG
AGCTGAGCAACTGAACCTGAAACTCTTCCACTGTGAGTCAAGGAGGCTTTTCCGCACATG
AAGGACGCTGAGCGGGAAGGACTCCTCTCTGCCTGCAGTTGTAGCGAGTGGACCAGCACC
AGGGGCTCTCTAGACTGCCCCTCCTCCATCGCCTTCCCTGCCTCTCCAGGACAGAGCAGC
CACGTCTGCACACCTCGCCCTCTTTACACTCAGTTTTCAGAGCACGTTTCTCCTATTTCC
TGCGGGTTGCAGCGCCTACTTGAACTTACTCAGACCACCTACTTCTCTAGCAGCACTGGG
CGTCCCTTTCAGCAAGACGATGGCTGTGCTCAGGCAGCTGGCGCTCCTCCTCTGGAAGAA
CTACACCCTGCAGAAGCGGAAGGTCCTGGTGACGGTCCTGGAACTCTTCCTGCCATTGCT
GTTTCCTGGGATCCTCATCTGGCTCCGCTTGAAGATTCAGTCGGAAAATGTGCCCAACGC
CACCATCTACCCGGGCCAGTCCATCCAGGAGCTGCCTCTGTTCTTCACCTTCCCTCCGCC
AGGAGACACCTGGGAGCTTGCCTACATCCCTTCTCACAGTGACGCTGCCAAGACCGTCAC
TGAGACAGTGCGCAGGGCACTTGTGATCAACATGCGAGTGCGCGGCTTTCCCTCCGAGAA
GGACTTTGAGGACTACATTAGGTACGACAACTGCTCGTCCAGCGTGCTGGCCGCCGTGGT

CTTCGAGCACCCCTTCAACCACAGCAAGGAGCCCCTGCCGCTGGCGGTGAAATATCACCT
ACGGTTCAGTTACACACGGAGAAATTACATGTGGACCCAAACAGGCTCCTTTTTCCTGAA
AGAGACAGAAGGCTGGCACACTACTTCCCTTTTCCCGCTTTTCCCAAACCCAGGACCAAG
GGAACTAACATCCCCTGATGGCGGAGAACCTGGGTACATCCGGGAAGGCTTCCTGGCCGT
GCAGCATGCTGTGGACCGGGCCATCATGGAGTACCATGCCGATGCCGCCACACGCCAGCT
GTTCCAGAGACTGACGGTGACCATCAAGAGGTTCCCGTACCCGCCGTTCATCGCAGACCC
CTTCCTCGTGGCCATCCAGTACCAGCTGCCCCTGCTGCTGCTGCTCAGCTTCACCTACAC
CGCGCTCACCATTGCCCGTGCTGTCGTGCAGGAGAAGGAAAGGAGGCTGAAGGAGTACAT
GCGCATGATGGGGCTCAGCAGCTGGCTGCACTGGAGTGCCTGGTTCCTCTTGTTCTTCCT
CTTCCTCCTCATCGCCGCCTCCTTCATGACCCTGCTCTTCTGTGTCAAGGTGAAGCCAAA
TGTAGCCGTGCTGTCCCGCAGCGACCCCTCCCTGGTGCTCGCCTTCCTGCTGTGCTTCGC
CATCTCTACCATCTCCTTCAGCTTCATGGTCAGCACCTTCTTCAGCAAAGCCAACATGGC
AGCAGCCTTCGGAGGCTTCCTCTACTTCTTCACCTACATCCCCTACTTCTTCGTGGCCCC
TCGGTACAACTGGATGACTCTGAGCCAGAAGCTCTGCTCCTGCCTCCTGTCTAATGTCGC
CATGGCAATGGGAGCCCAGCTCATTGGGAAATTTGAGGCGAAAGGCATGGGCATCCAGTG
GCGAGACCTCCTGAGTCCCGTCAACGTGGACGACGACTTCTGCTTCGGGCAGGTGCTGGG
GATGCTGCTGCTGGACTCTGTGCTCTATGGCCTGGTGACCTGGTACATGGAGGCCGTCTT
CCCAGGGCAGTTCGGCGTGCCTCAGCCCTGGTACTTCTTCATCATGCCCTCCTATTGGTG
TGGGAAGCCAAGGGCGGTTGCAGGGAAGGAGGAAGAAGACAGTGACCCCGAGAAAGCACT
CAGAAACGAGTACTTTGAAGCCGAGCCAGAGGACCTGGTGGCGGGGATCAAGATCAAGCA
CCTGTCCAAGGTGTTCAGGGTGGGAAATAAGGACAGGGCGGCCGTCAGAGACCTGAACCT
CAACCTGTACGAGGGACAGATCACCGTCCTGCTGGGCCACAACGGTGCCGGGAAGACCAC
CACCCTCTCCATGCTCACAGGTCTCTTTCCCCCCACCAGTGGACGGGCATACATCAGCGG
GTATGAAATTTCCCAGGACATGGTTCAGATCCGGAAGAGCCTGGGCCTGTGCCCGCAGCA
CGACATCCTGTTTGACAACTTGACAGTCGCAGAGCACCTTTATTTCTACGCCCAGCTGAA
GGGCCTGTCACGTCAGAAGTGCCCTGAAGAAGTCAAGCAGATGCTGCACATCATCGGCCT
GGAGGACAAGTGGAACTCACGGAGCCGCTTCCTGAGCGGGGGCATGAGGCGCAAGCTCTC
CATCGGCATCGCCCTCATCGCAGGCTCCAAGGTGCTGATACTGGACGAGCCCACCTCGGG
CATGGACGCCATCTCCAGGAGGGCCATCTGGGATCTTCTTCAGCGGCAGAAAAGTGACCG
CACCATCGTGCTGACCACCCACTTCATGGACGAGGCTGACCTGCTGGGAGACCGCATCGC
CATCATGGCCAAGGGGGAGCTGCAGTGCTGCGGGTCCTCGCTGTTCCTCAAGCAGAAATA
CGGTGCCGGCTATCACATGACGCTGGTGAAGGAGCCGCACTGCAACCCGGAAGACATCTC
CCAGCTGGTCCACCACCACGTGCCCAACGCCACGCTGGAGAGCAGCGCTGGGGCCGAGCT
GTCTTTCATCCTTCCCAGAGAGAGCACGCACAGGTTTGAAGGTCTCTTTGCTAAACTGGA
GAAGAAGCAGAAAGAGCTGGGCATTGCCAGCTTTGGGGCATCCATCACCACCATGGAGGA
AGTCTTCCTTCGGGTCGGGAAGCTGGTGGACAGCAGTATGGACATCCAGGCCATCCAGCT
CCCTGCCCTGCAGTACCAGCACGAGAGGCGCGCCAGCGACTGGGCTGTGGACAGCAACCT
CTGTGGGGCCATGGACCCCTCCGACGGCATTGGAGCCCTCATCGAGGAGGAGCGCACCGC
TGTCAAGCTCAACACTGGGCTCGCCCTGCACTGCCAGCAATTCTGGGCCATGTTCCTGAA

GAAGGCCGCATACAGCTGGCGCGAGTGGAAAATGGTGGCGGCACAGGTCCTGGTGCCTCT

GACCTGCGTCACCCTGGCCCTCCTGGCCATCAACTACTCCTCGGAGCTCTTCGACGACCC

CATGCTGAGGCTGACCTTGGGCGAGTACGGCAGAACCGTCGTGCCCTTCTCAGTTCCCGG

GACCTCCCAGCTGGGTCAGCAGCTGTCAGAGCATCTGAAAGACGCACTGCAGGCTGAGGG

ACAGGAGCCCCGCGAGGTGCTCGGTGACCTGGAGGAGTTCTTGATCTTCAGGGCTTCTGT

GGAGGGGGGCGGCTTTAATGAGCGGTGCCTTGTGGCAGCGTCCTTCAGAGATGTGGGAGA

GCGCACGGTCGTCAACGCCTTGTTCAACAACCAGGCGTACCACTCTCCAGCCACTGCCCT

GGCCGTCGTGGACAACCTTCTGTTCAAGCTGCTGTGCGGGCCTCACGCCTCCATTGTGGT

CTCCAACTTCCCCCAGCCCCGGAGCGCCCTGCAGGCTGCCAAGGACCAGTTTAACGAGGG

CCGGAAGGGATTCGACATTGCCCTCAACCTGCTCTTCGCCATGGCATTCTTGGCCAGCAC

GTTCTCCATCCTGGCGGTCAGCGAGAGGGCCGTGCAGGCCAAGCATGTGCAGTTTGTGAG

TGGAGTCCACGTGGCCAGTTTCTGGCTCTCTGCTCTGCTGTGGGACCTCATCTCCTTCCT

CATCCCCAGTCTGCTGCTGCTGGTGGTGTTTAAGGCCTTCGACGTGCGTGCCTTCACGCG

GGACGGCCACATGGCTGACACCCTGCTGCTGCTCCTGCTCTACGGCTGGGCCATCATCCC

CCTCATGTACCTGATGAACTTCTTCTTCTTGGGGGCGGCCACTGCCTACACGAGGCTGAC

CATCTTCAACATCCTGTCAGGCATCGCCACCTTCCTGATGGTCACCATCATGCGCATCCC

AGCTGTAAAACTGGAAGAACTTTCCAAAACCCTGGATCACGTGTTCCTGGTGCTGCCCAA

CCACTGTCTGGGGATGGCAGTCAGCAGTTTCTACGAGAACTACGAGACGCGGAGGTACTG

CACCTCCTCCGAGGTCGCCGCCCACTACTGCAAGAAATATAACATCCAGTACCAGGAGAA

CTTCTATGCCTGGAGCGCCCCGGGGGTCGGCCGGTTTGTGGCCTCCATGGCCGCCTCAGG

GTGCGCCTACCTCATCCTGCTCTTCCTCATCGAGACCAACCTGCTTCAGAGACTCAGGGG

CATCCTCTGCGCCCTCCGGAGGAGGCGGACACTGACAGAATTATACACCCGGATGCCTGT

GCTTCCTGAGGACCAAGATGTAGCGGACGAGAGGACCCGCATCCTGGCCCCCAGCCCGGA

CTCCCTGCTCCACACACCTCTGATTATCAAGGAGCTCTCCAAGGTGTACGAGCAGCGGGT

GCCCCTCCTGGCCGTGGACAGGCTCTCCCTCGCGGTGCAGAAAGGGGAGTGCTTCGGCCT

GCTGGGCTTCAATGGAGCCGGGAAGACCACGACTTTCAAAATGCTGACCGGGGAGGAGAG

CCTCACTTCTGGGGATGCCTTTGTCGGGGGTCACAGAATCAGCTCTGATGTCGGAAAGGT

GCGGCAGCGGATCGGCTACTGCCCGCAGTTTGATGCCTTGCTGGACCACATGACAGGCCG

GGAGATGCTGGTCATGTACGCTCGGCTCCGGGGCATCCCTGAGCGCCACATCGGGGCCTG

CGTGGAGAACACTCTGCGGGGCCTGCTGCTGGAGCCACATGCCAACAAGCTGGTCAGGAC

GTACAGTGGTGGTAACAAGCGGAAGCTGAGCACCGGCATCGCCCTGATCGGAGAGCCTGC

TGTCATCTTCCTGGACGAGCCGTCCACTGGCATGGACCCCGTGGCCCGGCGCCTGCTTTG

GGACACCGTGGCACGAGCCCGAGAGTCTGGCAAGGCCATCATCATCACCTCCCACAGCAT

GGAGGAGTGTGAGGCCCTGTGCACCCGGCTGGCCATCATGGTGCAGGGGCAGTTCAAGTG

CCTGGGCAGCCCCCAGCACCTCAAGAGCAAGTTCGGCAGCGGCTACTCCCTGCGGGCCAA

GGTGCAGAGTGAAGGGCAACAGGAGGCGCTGGAGGAGTTCAAGGCCTTCGTGGACCTGAC

CTTTCCAGGCAGCGTCCTGGAAGATGAGCACCAAGGCATGGTCCATTACCACCTGCCGGG

CCGTGACCTCAGCTGGGCGAAGGTTTTCGGTATTCTGGAGAAAGCCAAGGAAAAGTACGG

CGTGGACGACTACTCCGTGAGCCAGATCTCGCTGGAACAGGTCTTCCTGAGCTTCGCCCA

SUBSTITUTE SHEET (RULE 26)

CCTGCAGCCGCCCACCGCAGAGGAGGGGCGATGAGGGGTGGCGGCTGTCTCGCCATCAGG
CAGGGACAGGACGGGCAAGCAGGGCCCATCTTACATCCTCTCTCTCCAAGTTTATCTCAT
CCTTTATTTTTAATCACTTTTTTCTATGATGGATATGAAAAATTCAAGGCAGTATGCACA
GAATGGACGAGTGCAGCCCAGCCCTCATGCCCAGGATCAGCATGCGCATCTCCATGTCTG
CATACTCTGGAGTTCACTTTCCCAGAGCTGGGGCAGGCCGGGCAGTCTGCGGGCAAGCTC
CGGGGTCTCTGGGTGGAGAGCTGACCCAGGAAGGGCTGCAGCTGAGCTGGGGGTTGAATT
TCTCCAGGCACTCCCTGGAGAGAGGACCCAGTGACTTGTCCAAGTTTACACACGACACTA
ATCTCCCCTGGGGAGGAAGCGGGAAGCCAGCCAGGTTGAACTGTAGCGAGGCCCCCAGGC
CGCCAGGAATGGACCATGCAGATCACTGTCAGTGGAGGGAAGCTGCTGACTGTGATTAGG
TGCTGGGGTCTTAGCGTCCAGCGCAGCCCGGGGGCATCCTGGAGGCTCTGCTCCCTTAGG
GCATGGTAGTCACCGCGAAGCCGGGCACCGTCCCACAGCATCTCCTAGAAGCAGCCGGCA
CAGGAGGGAAGGTGGCCAGGCTCGAAGCAGTCTCTGTTTCCAGCACTGCACCCTCAGGAA
GTCGCCCGCCCCAGGACACGCAGGGACCACCCTAAGGGCTGGGTGGCTGTCTCAAGGACA
CATTGAATACGTTGTGACCATCCAGAAAATAAATGCTGAGGGGACACAAAAAAAAAAAAA
AAAAAAAAAAA

Fragment 640918

1 GAGATCCTGAGGCTTTTCCCCCAGGCTGCTCAGCAGGAAAGGTTCTCCTCCCTGATGGTC
61 TATAAGTTGCCTGTTGAGGATGTGCGACCTTTATCACAGGCTTTCTTCAAATTAGAGATA
121 GTTAAACAGAGTTTCGACCTGGAGGAGTACAGCCTCTCACAGTCTACCCTGGAGCAGGTT
181 TTCCTGGAGCTCTCCAAGGAGCAGGAGCTGGGTGATCTTGAAGAGGACTTTGATCCCTCG
241 GTGAAGTGGAAACTCCTCCTGCAGGAAGAGCCTTAAAGCTCCAAATACCCTATATCTTTC
301 TTTAATCCTGTGACTCTTTTAAAGATAATATTTTATAGCCTTAATATGCCTTATATCAGA
361 GGTGGTACAAAATGCATTTGAAACTCATGCAATAATTATC

Fragment 698739

1 GCTCTCCACACAGAGATTTTGAAGCTTTTCCCACAGGCTGCTTGGCAGGAAAGATATTCC
61 TCTTTAATGGCGTATAAGTTACCTGTGGAGGATGTCCACCCTCTATCTCGGGCCTTTTTC
121 AAGTTAGAGGCGATGAAACAGACCTTCAACCTGGAGGAATACAGCCTCTCTCAGGCTACC
181 TTGGAGCAGGTATTCTTAGAACTCTGTAAAGAGCAGGAGCTGGGAAATGTTGATGATAAA
241 ATTGATACAACAGTTGAATGGAAACTTCTCCCACAGGAAGACCCTTAAAATGAAGAACCT
301 CCTAACATTCAATTTTAGGTCCTACTACATTGTTAGTTTCCATAATTCTACAAGAATGTT
361 TCCTTTTACTTCAGTTAACAAAAGAAAACATTTAATAAACATTCAATAATGATTACAGTT
421 TTCATTTTTAAAAATTTAGGATGAAGGAAACAAGGAAATATAGGGAAAAGTAGTAGACAA
481 AATTAACAAAATCAGACATGTTATTCATCCCCAACATGGGTCTATTTTGTGCTTAAAAAT
541 AATTTAAAAATCATACAATATTAGGTTGGTTATCG

Fragment 990006

1 GTGGAAGATGTGCAACCTTTAGCCCAAGCTTTCTTCAAATTAGAGAAGGTTAAACAGAGC
61 TTTGACCTAGAGGAGTACAGCCTCTCACAGTCTACCCTGGAGCAGGTTTTCCTGGAGCTC
121 TCCAAGGAGCAGGAGCTGGGTGATTTTGAGGAGGATTTTGATCCCTCAGTGAAGTGGAAG

SUBSTITUTE SHEET (RULE 26)

181 CTCCTCCCCCAGGAAGAGCCTTAAAACCCCAAATTCTGTGTTCCTGTTTAAACCCGTGGT

241 TTTTTTTAAATACATTTATTTTTATAGCAGCAATGTTCTATTTTTAGAAACTATATTATA

Fragment 1133530

1 TTTTCAGTTG CATGTAATAC CAAGAAATCG AATTGTTTTC CGGTTCTTAT

51 GGGAATTGTT AGCAATGCCC TTATTGGAAT TTTTAACTTC ACAGAGCTTA

101 TTCAAATGGA GAGCACCTTA TTTTTTCGTG ATGACATAGT GCTGGATCTT

151 GGTTTTATAG ATGGGTCCAT ATTTTTGTTG TTGATCACAA ACTGCATTTC

201 TCCTTATATT GGCATAAGCA GCATCAGTGA TTATT

Fragment 1125168

CTGGATT

TGCTCTGCGG CAAGACCCGC GCCACCAGCG GCAGTATCCA GTTCGACGGC

CAGGAACTGA CCAAAATGCG CGAATACAAC ATCGTGCGGG CCGGGGTAGG

GCGCAAGTTT CAGAACCCGT CGATCTACGA AAACCTCACG GTGTTTGAAA

ACCTTGAGAT GTCTTATCCG GCTGGGCGCA AGGTCTGGGG TGCGCTGTTT

TTCAAGCGCA ATGCCCAGGT GGTGGCGCGG GTCGAG

Fragment 1203215

1 ATCGCCGATA TCTCCCCTTC GGGCTGCGGC AAGAGCACCT TCCTGAAAGT

51 GCTCGCCGGG TTCTATGCCC TGGACACCGG GCGCTTCAGG ATCAACGGCC

101 AGGCGATGCG GCATTTCGGT TTGCGCTCGT ACCGCCAGAG CGTGGCCTAT

151 GTCACGGCCC ACGACGAGAT CATCGCCGGG ACGGTGATCG AGAACATCCT

201 GATGGACAGC GACCCGCTGG ACGGCACGGG TTTGCAGAGC TGTGTCGAGC

251 AGGCCGGGTT GCTGGAAAGC ATCCTGAAAC TGAGCAATGG CTTCAATACC

301 TTGCTCGGAC CCATGGGCGT GCAATTGTCC TCGGGCCAGA AGCAACGCCT

351 GTTGATCGCC CGGGGTCGAC GC

Fragment 168043

1 AAAACCAAAG ATTCTCCTGG AGTTTTCTCT AAACTGGGTG TTCTCCTGAG

51 GAGAGTTGAC AAGAAACTTG GTGAGAAATA AGCTGGCAGT GATTACGCGT

101 CTCCTTCAGA ATCTGATCAT GGGTTTGTTC CTCCTTTTCT TCGTTCTGCG

151 GGTCCGAAGC AATGTGCTAA AGGGTGCTAT CCAGGACCGC GTAGGTCTCC

201 TTTACCAGTT TGTGGGCGCC ACCCCGTACA CAGGCATGCT GAACGCTGTG

251 AATCTGTTTC CCGTGCTGCG AGCTGTCAGC A

Huwhite2

1 ATGGCCGTGA CGCTGGAGGA CGGGGCGGAA CCCCCTGTGC TGACCACGCA

51 CCTGAAGAAG GTGGAGAACC ACATCACTGA AGCCCAGCGC TTCTCCCACC

101 TGCCCAAGCG CTCAGCCGTG GACATCGAGT TCGTGGAGCT GTCCTATTCC

151 GTGCGGGAGG GGCCCTGCTG GCGCAAAAGG GGTTATAAGA CCCTTCTCAA

201 GTGCCTCTCA GGTAAATTCT GCCGCCGGGA GCTGATTGGC ATCATGGGCC

251 CCTCAGGGGC TGGCAAGTCT ACATTCATGA ACATCTTGGC AGGATACAGG

301 GAGTCTGGAA TGAAGGGGCA GATCCTGGTT AATGGAAGGC CACGGGAGCT

SUBSTITUTE SHEET (RULE 26)

```
351  GAGGACCTTC CGCAAGATGT CCTGCTACAT CATGCAAGAT GACATGCTGC
401  TGCCGCACCT CACGGTGTTG GAAGCCATGA TGGTCTCTGC TAACCTGAAT
451  CTTACTGAGA ATCCCGATGT GAAAAACGAT CTCGTGACAG AGATCCTGAC
501  GGCACTGGGC CTGATGTCGT GCTCCCACAC GAGGACAGCC CTGCTCTCTG
551  GCGGGCAGAG GAAGCGTCTG GCCATCGCCC TGGAGCTGGT CAACAACCCG
601  CCTGTCATGT TCTTTGATGA GCCCACCAGT GGTCTGGATA GCGCCTCTTG
651  TTTCCAAGTG GTGTCCCTCA TGAAGTCCCT GGCACAGGGG GGCCGTACCA
701  TCATCTGCAC CATCCACCAG CCCAGTGCCA AGCTCTTTGA GATGTTTGAC
751  AAGCTCTACA TCCTGAGCCA GGGTCAGTGC ATCTTCAAAG GCGTGGTCAC
801  CAACCTGATC CCCTATCTAA AGGGACTCGG CTTGCATTGC CCCACCTACC
851  ACAACCCGGC TGACTTCAGT GAGTGGGGGT CTGTTGCCTC TGGCGAGTAT
901  GGACACCTGA ACCCCATGTT GTTCAGGGCT GTGCAGAATG GGCTGTGCGC
951  TATGGCTGAG AAGAAGAGCA GCCCTGAGAA GAACGAGGTC CCTGCCCCAT
1001 GCCCTCCTTG TCCTCCGGAA GTGGATCCCA TTGAAAGCCA CACCTTTGCC
1051 ACCAGCACCC TCACACAGTT CTGCATCCTC TTCAAGAGGA CCTTCCTGTC
1101 CATCCTCAGG GACACGGTCC TGACCCACCT ACGGTTCATG TCCCACGTGG
1151 TTATTGGCGT GCTCATCGGC CTCCTCTACC TGCATATTGG CGACGATGCC
1201 AGCAAGGTCT TCAACAACAC CGGCTGCCTC TTCTTCTCCA TGCTGTTCCT
1251 CATGTTCGCC GCCCTCATGC CAACTGTGCT CACCTTCCCC TTAGAGATGG
1301 CGGTCTTCAT GAGGGAGCAC CTCAACTACT GGTACAGCCT CAAAGCGTAT
1351 TACCTGGCCA AGACCATGGC TGACGTGCCC TTTCAGGTGG TGTGTCCGGT
1401 GGTCTACTGC AGCATTGTGT ACTGGATGAA CGGCCAGCCC GCTGAGACCA
1451 GCCGCTTCCT GCTCTTCTCA GCCCTGGCCA CCGCCACCGC CTTGGTGGCC
1501 CAATCTTTGG GGCTGCTGAT CGGAGCTGCT TCCAACTCCC TACAGGTGGC
1551 CACTTTTGTG GGCCCAGTTA CCGCCATCCC TGTCCTCTTG TTCTCCGGCT
1601 TCTTTGTCAG CTTCAAGACC ATCCCCACTT ACCTGCAATG GAGCTCCTAT
1651 CTCTCCTATG TCAGGTATGG CTTTGAGGGT GTGATCCTGA CGATCTATGG
1701 CATGGAGCGA GGAGACCTGA CATGTTTAGA GGAACGCTGC CCGTTCCGGG
1751 AGCCACAGAG CATCCTCCGA GCGCTGGATG TGGAGGATGC CAAGCTCTAC
1801 ATGGACTTCC TGGTCTTGGG CATCTTCTTC CTAGCCCTGC GGCTGCTGGC
1851 CTACCTTGTG CTGCGTTACC GGGTCAAGTC AGAGAGATAG AGGCTTGCCC
1901 CAGCCTGTAC CCCAGCCCCT GCAGCAGGAA GCCCCCAGTC CCAGCCCTTT
1951 GGGACTGTTT TANCTCTATA CACTTGGGCA CTGGTTCCTG GCGGGGCTAT
2001 CCTCTCCTCC CTTGGCTCCT CCACAGGCTG GCTGTCGGAC TGCGCTCCCA
2051 GCCTGGGCTC TGGGAGTGGG GGCTCCAACC CTCCCCACTA TGCCCAGGAG
2101 TCTTCCCAAG TTGATGCGGT TTGTAGCTTC CTCCCTACTC TCTCCAACAC
2151 CTGCATGCAA AGACTACTGG GAGGCTGCTG CCTCCTTCCT GCCCATGGCA
2201 CCCTCCTCTG CTGTCTGCCT GGGAGCCCTA GGCTCTCTAT GGCCCCACTT
2251 ACAACTGA
```

SUBSTITUTE SHEET (RULE 26)

Fragment 20237

```
   1 TTTAAGGATT TCAGCCTTTC CATTCCGTCA GGATCTGTCA CGGCACTGGT TGGCCCAAGT
  61 GGTTCTGGCA AATCAACAGT GCTTTCACTC CTGCTGAGGT TGTACGACCC TGCTTCTGGA
 121 ACTATTAGTC TTGATGGCCA TGACAATCCG TCAGCTAAAC CCAGTGTGTG GCTGAGATCC
 181 AAAATTGGGA CAGTCAGTCA GGAACCCATT TTGTTTTCTT GCTCTATTGC TGAGAACATT
 241 GCTTATGGTG CTGATGACCC TTCCTCTGTG ACCGCTGAGG AAATCCAGAG AGTGGCTGAA
 301 GTGGCCAATG CAGTGGCTTC TCCGGAATTT CCCCCAAGGT TCAACACTGT GGTTGGAGAA
 361 AAGGGTGTTC TCCTCTCAGG TGGGCAGAAA CAGCGGATTG CGATTGCCCG TGCTCTGCTA
 421 AAGAATCCCA AAATTCTTCT CCTAGATGAA GCAACCAGTG CGCTGGATGC CGAAAATGAG
 481 TACCTTGTTC AAGAAGCTCT AGATCGCCTG ATGGATGGAA GAACGGTGTT AGTTATTGCC
 541 CATAGCCTGT CCACCATTAA GAATGCTAAT ATGGTTGCTG TTCTTGACCA AGGAAAAATT
 601 ACTGAATATG GAAAACATGA AGAGCTGCTT TCAAAACCAA ATGGGATATA CAGAAAACTA
 661 ATGAACAAAC AAAGTTTTAT TTCAGCATAA GGAAGCAATT ACTGGTAAAC AATATGAGAC
 721 TTTAATGCAA AACAGTGTTG CGAAAAAAAA CTCAGAGACT ATGAAATACA TAAACCATAT
 781 ATCAAGTTAT TTGAAAAATA CCTATTTTTT CCAAAGTGTG
```

SUBSTITUTE SHEET (RULE 26)